

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 29, 2005, 20:02:31 ; Search time 154.23 Seconds
(without alignments)
7193.137 Million cell updates/sec

Title: US-10-081-864A-14

Perfect score: 678
Sequence: 1 atggccctcccgagaaagc.....gccacacactgtctctgtaa 678

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq: *
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq: *
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PTCUS_COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	655.2	96.6	723	US-10-152-296-1	Sequence 1, Appl1
2	438	64.6	678	US-09-459-956-6	Sequence 5, Appl1
3	257.4	38.0	699	US-09-459-956-5	Sequence 5, Appl1
4	251.8	37.1	720	US-09-839-650-1	Sequence 1, Appl1
5	245	36.1	1482	US-09-977-887-1	Sequence 1, Appl1
6	216.6	31.9	801	US-09-459-956-7	Sequence 7, Appl1
7	144.8	21.4	690	US-09-459-956-2	Sequence 2, Appl1
8	119	17.6	1104	US-09-277-716-30	Sequence 30, Appl1
9	119	17.6	1104	US-09-609-1618-30	Sequence 30, Appl1
10	119	17.6	1278	US-09-277-716-31	Sequence 31, Appl1
11	119	17.6	1279	US-09-609-1618-31	Sequence 31, Appl1
12	110.4	16.3	696	US-09-459-956-4	Sequence 4, Appl1
13	100.2	14.8	717	US-09-214-909-1	Sequence 1, Appl1
14	99.2	14.6	696	US-09-459-956-3	Sequence 3, Appl1
15	99	14.6	717	US-09-486-241-31	Sequence 31, Appl1
16	98.4	14.5	1079	US-09-609-1618-15	Sequence 15, Appl1
17	98.4	14.5	1079	US-09-626-581D-64	Sequence 64, Appl1
18	98.4	14.5	1079	US-09-415-765B-64	Sequence 64, Appl1
19	98.4	14.5	1079	US-09-626-580C-64	Sequence 64, Appl1
20	98.4	14.5	1085	US-09-277-716-15	Sequence 15, Appl1
21	95.2	14.0	1021	US-09-839-650-2	Sequence 2, Appl1
22	95.4	13.9	762	US-08-532-390-40	Sequence 40, Appl1
23	94.4	13.9	762	US-08-717-294-40	Sequence 40, Appl1
24	93	13.7	720	US-09-172-063-14	Sequence 14, Appl1
25	93	13.7	720	US-09-316-919-15	Sequence 15, Appl1
26	93	13.7	720	US-09-602-641-14	Sequence 14, Appl1
27	93	13.7	720	US-09-316-920A-15	Sequence 15, Appl1

28	92.8	13.7	7353	US-08-786-531B-1	Sequence 1, Appl1
29	91.4	13.5	717	US-09-513-783A-43	Sequence 43, Appl1
30	91.4	13.5	717	US-09-430-656-43	Sequence 43, Appl1
31	91.4	13.5	720	US-09-094-359-9	Sequence 9, Appl1
32	91.4	13.5	720	US-09-172-063-12	Sequence 12, Appl1
33	91.4	13.5	720	US-09-172-063-17	Sequence 17, Appl1
34	91.4	13.5	720	US-09-316-919-13	Sequence 13, Appl1
35	91.4	13.5	720	US-09-316-919-18	Sequence 18, Appl1
36	91.4	13.5	720	US-09-602-641-12	Sequence 12, Appl1
37	91.4	13.5	720	US-09-602-641-17	Sequence 17, Appl1
38	91.4	13.5	720	US-09-704-463-9	Sequence 9, Appl1
39	91.4	13.5	720	US-09-316-920A-13	Sequence 13, Appl1
40	91.4	13.5	720	US-09-316-920A-18	Sequence 18, Appl1
41	91.4	13.5	768	US-09-172-063-28	Sequence 28, Appl1
42	91.4	13.5	768	US-09-172-063-33	Sequence 33, Appl1
43	91.4	13.5	768	US-09-602-641-28	Sequence 28, Appl1
44	91.4	13.5	768	US-09-602-641-33	Sequence 33, Appl1
45	91.4	13.5	972	US-09-172-063-30	Sequence 30, Appl1

ALIGNMENTS

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RESULT 1
US-10-152-296-1
Sequence 1, Application US/10152296
Patent No. 6723537
GENERAL INFORMATION:
APPLICANT: Beele, Beau
TITLE OF INVENTION: Directed Evolution of Protein in Mammalian Cells
FILE REFERENCE: 021044-000110US
CURRENT APPLICATION NUMBER: US/10152,296
PRIORITY FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: US 60/291,871
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 723
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence:mammalian
OTHER INFORMATION: codon-optimized variant (DSRED) of Discosoma sp.
OTHER INFORMATION: "red" red fluorescent protein (RFP)
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(723)
OTHER INFORMATION: DSRED
US-10-152-296-1
Query Match 96.6%; Score 655.2; DB 4; Length 723;
Best Local Similarity 98.1%; Pred. No. 6.8e-125;
Matches 663; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
2 TGCGCTCTCCGAGAAGCTATCCAGAGTTCAGCGCTTAAAGTGGCATGAGGCA 61
5 TGCCTCTCCGAGAAGCTATCCAGAGTTCAGCGCTTAAAGTGGCATGAGGCA 64
62 CCGTGAACGGCAGAGTTCAGAGTTCAGAGGCGAGGCGAGGCGCCCTTACGAGGCGC 121
65 CCGTGAACGGCAGAGTTCAGAGTTCAGAGGCGAGGCGAGGCGCCCTTACGAGGCGC 124
122 ACAACACCGTGAAGTGAAGTGAACCAAGAGCGGCGCCCTTACGAGGCGCATCC 181
125 ACAACACCGTGAAGTGAAGTGAACCAAGAGCGGCGCCCTTACGAGGCGCATCC 184
182 TGTCCCGCCGAGTTCAGAGTTCAGAGTTCAGAGGCGAGGCGAGGCGCGAGGCGG 241
185 TGTCCCGCCGAGTTCAGAGTTCAGAGTTCAGAGGCGAGGCGAGGCGCGAGGCGG 244
242 ACTACAGAAGCTGTCTTCCCGAGGCGTTCAAGTGGAGCGCGTATGAATTCGAGG 301
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Db	245	ACTACAAAGCTGTCTTCTCCCGAGGCTTCAATGGAGCCGTGATGAATTCGAGG	304
Qy	302	ACGGCGGCGTGGCGAACCGTGAACCCAGAACTCTCTCTGAGGACGGCTGTCATCTACA	361b
Db	305	ACGGCGGCGTGGTGAACCGTGAACCCAGAACTCTCTCTGAGGACGGCTGTCATCTACA	364a
Qy	362	AGGTAAATTCATCGGCGTGAACTTCCCTCCGACGGCCCCGTGATGCAGAGAACCA	421b
Db	365	AGGTAAATTCATCGGCGTGAACTTCCCTCCGACGGCCCCGTGATGCAGAGAACCA	424a
Qy	422	TGGGCTGGGAGGCGCTCAACGAGCGCTGTATACCCCGGCGACGGCGGTGTGAAGGGGAGA	481b
Db	425	TGGGCTGGGAGGCGCTCAACGAGCGCTGTATACCCCGGCGACGGCGGTGTGAAGGGGAGA	484a
Qy	482	TCCACAAAGCCCTGGAAGCTGAAGACGCGGCGCACTACTGGTGGAGTTCAACTGCATCT	541b
Db	485	TCCACAAAGCCCTGGAAGCTGAAGAGCGGCGCACTACTGGTGGAGTTCAAAGTATCT	544a
Qy	542	ACATGGCCAAAGAGCCCGGTGACGTGCACCGGCTACTTACTACGTGACACCAAGCTGGACA	601b
Db	545	ACATGGCCAAAGAGCCCGGTGACGTGCACCGGCTACTTACTACGTGACCTCAACTGGACA	604a
Qy	602	TCACTTCCCAACAAGAGCTTACACCATCTGTGAGCATGACGACCCGAGGCGCGCC	661b
Db	605	TCACTTCCCAACAAGAGACTTACACCATCTGTGAGCATGACGACCCGAGGCGCGCC	664a
Qy	662	ACCACTGTCTCTGTA 677	
Db	665	ACCACTGTCTCTGGA 680	

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RESULT 2
US-09-459-956-6
; Sequence 6, Application US/09459956
; Patent No. 6342379
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Gonzalez, III, Jesus E.
; TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY
; TITLE OF INVENTION: OPTICAL METHODS
; FILE REFERENCE: REGEN1290-4
; CURRENT APPLICATION NUMBER: US/09/459,956
; PRIOR FILING DATE: 1993-12-13
; PRIOR APPLICATION NUMBER: 08/765,860
; PRIOR FILING DATE: 1999-05-08
; PRIOR APPLICATION NUMBER: 08/481,977
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: PCT/US96/09652
; PRIOR FILING DATE: 1996-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 678
; TYPE: DNA
; ORGANISM: Discosoma sp
; US-09-459-956-6

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Query Match	64.6%	Score 438	DB 3	Length 678
Best Local Similarity	77.9%	Pred. No. 1.4e-80		
Matches 528	Conservative 0	Mismatches 150	Indels 0	Gaps 0

Qy	Db	Qy	Db	Qy	Db	Qy	Db	Qy	Db
1	1	61	1	121	1	121	1	121	1
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60	60	120	120	180	180				

QY	181	CTGTCCCCCAGTTCCAGTAAAGGCTCAAGAGTACAGTAAGAACACCCCGCCGACATCCCC	240
Db	181	TTGTACCAACAATTTCAGTATAGAAAGCAAGATATGTACAGCACCCCTCCGACATACCA	240
QY	241	GACTACAAAGAACTGTCTCTCCCGAGAGGCTTCAAGTGAGACCGCGTATGAATCTTGAG	300
Db	241	GACTATTAAGCTCTCATTTCTCTGAAGATTAAATAGGAAGGGTCATGAACCTTTGAA	300
QY	301	GACGCGGCGATGAGCAGCCGTGACCGAGGACTCTCTCCCTGACAGACGGCGCTTCATCTAC	360
Db	301	GACGCTGGCGTCTGTTACTGTAAACCAAGATTTCAAGTTGACAGATAGCGTGTTCATCTAC	360
QY	361	AAAGTGAAGTTCATCGGCGGTGAATCTTCCCTTCGACGCGCCCGTATGACAGAAAGAAC	420
Db	361	AAAGTCAAGTTCAATGCGGTGAATCTTCCCTTCGATGACCTGTTATGCAGAAAGAACACA	420
QY	421	ATGGCGTGGGAGGCGCTCCACGAGGCGCCGTACCCCGCGAGAGGGGTGCTGAAGGCGAG	480
Db	421	ATGGCGTGGGAGGCGACGACTGAGGGTGTGTATCTCGTGAATGGCGGTGTGAAGAGAG	480
QY	481	ATCCCAAGAGCGCTTGAACTGAAAGACGCGCGCCACTACCTTGSTGAAGTTCAAGTCCATC	540
Db	481	ATTCTAATAGGCTCTGAAGCTGAAGAAGCGGTGGTCATTACTTAAGTTGAATTTCAAAAGTATT	540
QY	541	TACATGGCCAAAGAACCCGTGCAAGTGTGCCCGGCTCTCTACTAGTGAACCAAGCTGAC	600
Db	541	TACATGGCAAGAAACCTGTGAGCTTACCAAGGATCTACTATGTTGATCTTCAAACTGGAT	600
QY	601	ATCACTTCCCAACAGAGACTACACCAATCGTGAAGAGTACGAGCGCACCGAGGGCCGCG	660
Db	601	ATAACAAACCAACAGAGACTATATCATTCGTTGACGATATGAAGAAGAACCGAGGGACGC	660
QY	661	CACCACTGTTCCTGTAA 678	
Db	661	CACCATCTGTCTTTAA 678	

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RESULT 3
US-09-459-956-5
; Sequence 5, Application US/09459956
; Patent No. 6342379
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Gonzalez, Rita Jesus E.
; TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY
; TITLE OF INVENTION: OPTICAL METHODS
; FILE REFERENCE: REGEN1290-4
; CURRENT APPLICATION NUMBER: US/09/459,956
; CURRENT FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 08/765,860
; PRIOR FILING DATE: 1999-05-08
; PRIOR APPLICATION NUMBER: 08/481,977
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: PCT/US96/09652
; PRIOR FILING DATE: 1996-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 699
; TYPE: DNA
; ORGANISM: Discosoma striata
US-09-459-956-5

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Query Match	38.0%	Score 257.4;	DB 3,	Length 699;
Best Local Similarity	62.4%;	Pred. No. 9.4e-44;		
Matches 421; Conservative	0;	Mismatches 251;	Indels 3;	Gaps 1;

61 ACCGTGAA CGGCGCAGAGTT CGAGATCGAGGGCGAGGGCGCGCCCTTACGAGGCG 120

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Db 61 ACCTTCATGGGCACTACTTGAATTAAGGCAAGGAAAGGAGACAGCTTAATGAAGC 120
Qy 121 CACAACACCGTGAAGTTGAAGTGACCAAGGCGCGCCCTGCTGCTGGGAATC 180
Db 121 ACCAATACCGTCAAGGTTACCAAGGTTGACCTCTCCATTGGTGGCATATT 180
Qy 181 CTTGCTCCCAATTCAGTATGAGGCTCCCAAGGTTGATGTAAGCAACCCCGCAATCCC 240
Db 181 TTGTCCCAATTCAGTATGAGGCTCCCAAGGTTGATGTAAGCAACCCCGCAATCAT 240
Qy 241 GACTCAAGAAAGCTGCTCTCCCGAGGCTTCAAGTGGAGCGGCTGATGAATCTCGAG 300
Db 241 GATTTCATTAAGCTGCTATTTCCGAGGAGATATACATGGGAACGGTCCATGCACTTTGA 300
Qy 301 GAGGCGGCGGTGGCAACCGTGACCAAGACTCTCTCCCTGAGAGACGGCTGCTTCAATAC 360
Db 301 GACGGTGGCTTGTGTGTATCAACCAATGATATCAGTTGACAGGCAACTGTTCTACTAC 360
Qy 361 AAGGTGAAGTTGATGGCGGTGAACCTCCCTCCAGCGCGCGGTGATGAGAAAGACC 420
Db 361 GACATCAAGTTCACTGGCTTGAACCTTCTCCAAATGACCGGTGTGCAAGAAAGACA 420
Qy 421 ATGGGCTGGAGAGGCTCCACCGAGCGCTGTACCCCGGAGCGGCTGTAAGGCGAG 480
Db 421 ACTGGCTGGGAACCGAGCACTGAGCGTTGTATCTCGTGAATGTGTGTATGAGAGAC 480
Qy 481 ATCCACAAAGGCGCTGAAGCTGAAGAGCGGCGCACTACCTGTGAGTGAATGATCCATC 540
Db 481 ATCCATCATGCTCTGACAGTTGAAGAGGTGTCAATTACGATGACATTTAAACTGTT 540
Qy 541 TACATGCGCCAAAGACCGG---TGACGCTGCCGCTACTACTAGGTGACCAAGCTG 597
Db 541 TACAGGCGCCAAAGACCGGCTTGAAGATGCGAGGATACACTAGTGTACCAAACTG 600
Qy 598 GACATCACTCCCAAGAGAGACTACACATCTGTGAGAGCACTAGAGCGACCGAGGAC 657
Db 601 GTTATATGGAACAAAGCAAAATTCATGAAGTTGAGAGCAATGAATCCCGTTGCA 660
Qy 658 CGCCACCAACTGTTC 672
Db 661 CGCCACCAACTCGTTC 675
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RESULT 4
US-09-839-650-1
; Sequence 1, Application US/09839650
; Patent No. 6645761
; GENERAL INFORMATION:
; APPLICANT: Stratagene
; TITLE OF INVENTION: Humanized Polynucleotide Sequence Encoding Renilla Mulleri Green
; Patent No. 6645761
; TITLE OF INVENTION: Fluorescent Protein
; FILE REFERENCE: 25436/1755
; CURRENT APPLICATION NUMBER: US/09/839,650
; CURRENT FILING DATE: 2001-04-19
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized R. mulleri polynucleotide
; NAME/KEY: misc. feature
; LOCATION: (1)..(720)
; OTHER INFORMATION: Humanized DNA sequence
US-09-839-650-1
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Query Match 37.1%; Score 251.8; DB 4; Length 720;
Best Local Similarity 62.4%; Pred. No. 1.3e-42;
Matches 394; Conservative 0; Mismatches 237; Indels 0; Gaps 0;

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Qy 28 GAGTTCATGCGCTTCAAGATGCGATGAGAGGCAACCGTGAACGCGCAAGTTGAGATC 87
Db 40 GAGGTGATGAGCTTACAGATGAACTTGAAGGCACTGTGAACACAGCTGTTCACATG 99
Qy 88 GAGGCGAGGCGAGGCGCGCCCTTACAGAGGCGCAACAACCGTGAAGTTGAAGTGACC 147
Db 100 GAGGCTGCGGCAAGGCGCAACATCTGTTCGCAACAGCTGTGTCAGATTCGCGGTGACC 159
Qy 148 AAGGGCGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 207
Db 160 AAGGGCGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 219
Qy 208 AAGGTGATGATGAGACCGCGCGATCCCGCACTCAAGAAAGCTGCTCTTCCCGAG 267
Db 220 CGACCTTACCAAGTACCCCAAGCAATCAGCGACTTCTTCAATCAGAGCTTCCCGCGC 279
Qy 268 GCGTTCAAGTGGAGACCGGCTGATGAATCTTCAAGAGCGGCGGTGAGCAACCGTGA 327
Db 280 GCGTTCAATGACAGCGCACCTGCGCTACAGAGACGCGCGGCTGTGGAATCCGCAAGC 339
Qy 328 GACTCTCTCTGCAAGAGGCTGCTTCAATCTTCAAGTGAAGTTGATGAGGCTGAATTC 387
Db 340 GACATCAACTGATGAGAGCAAGTTCGTATACCGCGTGAAGTACAAAGGCGCAACTTC 399
Qy 388 CCTCCGACGCGCGCGGTGATGAGAAAGACCATGGGCTGGAGGCTCCACCGAGCGC 447
Db 400 CCGAGAGCGCGCGCGGTGATGAGAAAGACCATCTGGGCTATGAGCCAGCTTCCAGGCGC 459
Qy 448 CTGTACCCCGCGAGCGGCTGTGAAGGCGAGATCCAAAGGCCCTGAAGCTGAAGAC 507
Db 460 ATGTATATGAACAAGCGGCTGTGAGGCGAGGTGATCTGTGTATCAAGCTGAACAGC 519
Qy 508 GCGGCGCACTACCTGCTGAGATTCATGATCTATCATATGAGCCAGACCGCTGAGCTG 567
Db 520 GCGAAGTACTACGCTGCGCAATGAAGACCTGATGAAGAGAGAGCGGCTGTGAAGAG 579
Qy 568 CCGGCTACTACTAGTGAAGCAACAAAGCTGACATCCTCCCAAGAGAGACTACACC 627
Db 580 TTCCCTCTTCACTTATTCAGCAACCGCTGGAAGAAAGCTTACGTGAGAGACGGCGGC 639
Qy 628 ATCGTGAAGATGAGCGGACCGAGGAGCC 658
Db 640 TTGCTGAGAGAGCAAGAGACCGGCAATCGCCC 670
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RESULT 5
US-09-977-897-1
; Sequence 1, Application US/09977897
; Patent No. 6780974
; GENERAL INFORMATION:
; APPLICANT: Chem. Yih-Tai
; TITLE OF INVENTION: A synthetic DNA encoding an orange seapen-derived green fluorescence
; TITLE OF INVENTION: Protein with codon preference of mammalian expression systems ar
; FILE REFERENCE: 41856-5
; CURRENT APPLICATION NUMBER: US/09/977,897
; CURRENT FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1482
; TYPE: DNA
; ORGANISM: Peliosarcus gurneyi
US-09-977-897-1
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Query Match 36.1%; Score 245; DB 4; Length 1482;
Best Local Similarity 61.2%; Pred. No. 3.5e-41;
Matches 395; Conservative 0; Mismatches 250; Indels 0; Gaps 0;

Db	122	CCACCATGGGTGTGATTAAACCAAGACATGAAGATTAAAGTGAAGTGAAGAAATGTAA	181
Qy	68	ACGGCACGAGAGTTTCAGAGATCGAGGGCGAGGGCGCGCCGCCCTTACGAGGGCCACAAC	127
Db	182	ACGGGCATGCTTTTGTGATTCGAAGGAGAAAGAAAGAAAGCTTATCGATGGGACACAC	241
Qy	128	CCGTGAAGTTGAAGGTGACCAAGGGCGGCCCTCTGCTTCCGCTGGGACATCTCTTCCC	187
Db	242	CTTTAAACCTGGAAATGGAAGGAGTGGCCCTCTGCTTTTCTTAACGATATCTGTGCA	301
Qy	188	CCCAATTCACAGTACGGCTTCAGAGTGTACGTGAAGACACCCGCGGACATCCCGCATTACA	247
Db	302	ACGCTTTCAGTACGGAAGAAAGACGATTCGACAAATATCCCAAGCATATAGCAGACTATT	361
Qy	248	AGAACTGTCTTCCCGAGGGCTTCAAGTGGAGCGCGTATGAACTTTCAGAGACGGCG	307
Db	362	TCAAACAGATCGTTTCCGAGGGATATTCTCTGGGAAAGAACATATGACTTTTGAAGACAAAG	421
Qy	308	GGGTGGGACCGTGAACCGAGATCTCTCCCTGACAGACGGCGTGCATTACCTCAAGGTGA	367
Db	422	GGATTGTCAAAATGAAAAGTAGCATTAAGATGGAAGAAACATCTTTATCTATGAAATTC	481
Qy	368	AGTTTCATCGGCGTGAATCTTCCCTTCGACGCGCCCGCTGATGACGAAGAAAGACCATGGCT	427
Db	482	GTTTTCATGGGATGAATCTTCTCCCAATGGTCCGGTTATGCAAGAAAAAACTTTGAAGT	541
Qy	428	GGGAGGCTCCACCGACGCGCTGTATCCCCCGGACGCGCGTGTGAAGGGCGGATTCACA	487
Db	542	GGGAACCATTCACATGAGATTATATACGTGCGTGAAGTGGAGTGTGCGAGATATTAAGCC	601
Qy	488	AGGCGCTTAAGGTGAAGACGGCGGCGCATACCTGATGGAGTTCAAGTCCATCTACATGG	547
Db	602	ATTCTCTGTGTGAGGGGAGGTGGCCATTACCGATGTGACTTCAAAAGTATTTACAAAG	661
Qy	548	CCAAAGAACCCGCTGACGCTGCGCGGCTACTACTACGTGACACCAAGCTGACATCACCT	607
Db	662	CAAAAAAAGTTGTCAAAATTGCGAAGCTATCACTTTGTGGACATGCGATTTGATCTTGA	721
Qy	608	CCCACAAACGAGAGATCACCAATCTGTGGAGCAAGTACGAGCGCACCGAGGGCGGCCA	662
Db	722	ACCAATGACAAAGATTAACAACAAGTAAAGCTGTATGAAGATTCGAATTTGCTGCTTA	776

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RESULT 7
US-09-459-956-2
; Sequence 2, Application US/09459956
; Patent No. 6342379
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY
; TITLE OF INVENTION: OPTICAL METHODS
; FILE REFERENCE: REGEN1290-4
; CURRENT APPLICATION NUMBER: US/09/459, 956
; CURRENT FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 08/765, 860
; PRIOR FILING DATE: 1999-05-08
; PRIOR APPLICATION NUMBER: 08/481, 977
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: PCT/US96/09652
; PRIOR FILING DATE: 1996-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 690
; TYPE: DNA
; ORGANISM: Anemonia majano
US-09-459-956-2

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Query Match	21.4%	Score 144.8; DB 3;	Length 690;
Best Local Similarly	52.4%;	Pred. No. 8.7e-21;	
Matches 345; Conservative	0;	Mismatches 307;	Indels 6; Gaps 1

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QY 1 ATGGCTCTCCGAGAGCGATCAACGAGTTCAATGCGTTCAGAGGTGGCGAGGGC 60
Db 1 ATGGCTCTTTCAACAAGATTATCGAGATGACATGAATAATGCTCACTATGATGGC 60
QY 61 ACCGTGAACGCGCCACGAGTTTCAGATCGAGGCGAGGCGCGCCCTTACGAGGCG 120
Db 61 ACCGTGAACGCGCCACGAGTTTCAGATCGAGGCGAGGCGCGCCCTTACGAGGCG 120
QY 61 TGTGTCAATGGGCACTTACTTACCGTCGAAGGTGAAGGCAAGGAGGCATACGAGG 120
Db 61 TGTGTCAATGGGCACTTACTTACCGTCGAAGGTGAAGGCAAGGAGGCATACGAGG 120
QY 121 CACAACAACCGTGAAGTTGAAGGTGACCAAGGCG-----GGCCCCCTGCGCTTGG 174
Db 121 CACAACAACCGTGAAGTTGAAGGTGACCAAGGCG-----GGCCCCCTGCGCTTGG 174
QY 121 ACGCAGACTCTTCACTTTTAAAGTCACCATGCGCCACAGCGTGGGCGCCCTTCATTTCTTT 180
Db 121 ACGCAGACTCTTCACTTTTAAAGTCACCATGCGCCACAGCGTGGGCGCCCTTCATTTCTTT 180
QY 175 GACATCTGTGTCGCCCGAGTTCCAGTACGGCTCCAGGTGATGATGAAGACCCCGCGAC 234
Db 175 GACATCTGTGTCGCCCGAGTTCCAGTACGGCTCCAGGTGATGATGAAGACCCCGCGAC 234
QY 181 GACATCTGTGTCGCCCGAGTTCCAGTACGGCTCCAGGTGATGATGAAGACCCCGCGAC 240
Db 181 GACATCTGTGTCGCCCGAGTTCCAGTACGGCTCCAGGTGATGATGAAGACCCCGCGAC 240
QY 235 ATCCCGCATCAAGAGAGCTGTCTTCCCGAGGCGCTTCAGTGGAGCGCGTGAATGAC 294
Db 235 ATCCCGCATCAAGAGAGCTGTCTTCCCGAGGCGCTTCAGTGGAGCGCGTGAATGAC 294
QY 241 ATGCCCGACTATTTCACCAAGCATTTCTGACGGAATGTCATATGAAGACCTTTTACC 300
Db 241 ATGCCCGACTATTTCACCAAGCATTTCTGACGGAATGTCATATGAAGACCTTTTACC 300
QY 295 TTGAGAGACGCGCGGTGGCGACCGTGAACCCAGACTCTCCCTGAGAGACGGCTGCTTC 354
Db 295 TTGAGAGACGCGCGGTGGCGACCGTGAACCCAGACTCTCCCTGAGAGACGGCTGCTTC 354
QY 301 TATGAAGATGAGAGGTGCTACAGCCAGTTGGGAAATGAAGCCTTAAAGGCAACTGCTTT 360
Db 301 TATGAAGATGAGAGGTGCTACAGCCAGTTGGGAAATGAAGCCTTAAAGGCAACTGCTTT 360
QY 355 ATCTCAAGGTGAAGTTCAATGCGCGTGAACCTTCCCTCGAGGCGCGCGTGAATGACGAAG 414
Db 355 ATCTCAAGGTGAAGTTCAATGCGCGTGAACCTTCCCTCGAGGCGCGCGTGAATGACGAAG 414
QY 361 GAGCAACAATCCAGCTTTCATGATGAGTGAACCTTTCCTGATGATGACCTGTGATGGCGAAG 420
Db 361 GAGCAACAATCCAGCTTTCATGATGAGTGAACCTTTCCTGATGATGACCTGTGATGGCGAAG 420
QY 415 AAGACCATGGGCTGGAGAGCGCTCAACCGAGCGCTGTATCCCGCGCACGCGCTGTGAAG 474
Db 415 AAGACCATGGGCTGGAGAGCGCTCAACCGAGCGCTGTATCCCGCGCACGCGCTGTGAAG 474
QY 421 AAGACAACGTGTGGGACCCATCTTTTGAGAAATGACGTCTGGGATGGAATATTGAAG 480
Db 421 AAGACAACGTGTGGGACCCATCTTTTGAGAAATGACGTCTGGGATGGAATATTGAAG 480
QY 475 GCGGAGATCCACAGAGCCCTGAAGCTGAAGAGACGCGCGCCACTACTGCTGAGTTCAAG 534
Db 475 GCGGAGATCCACAGAGCCCTGAAGCTGAAGAGACGCGCGCCACTACTGCTGAGTTCAAG 534
QY 481 GGTGATGTCCACCGCTTCTCATGTCTGACAGAGGAGTGGCAATTAAGATGCCAATTTCCAC 540
Db 481 GGTGATGTCCACCGCTTCTCATGTCTGACAGAGGAGTGGCAATTAAGATGCCAATTTCCAC 540
QY 535 TCCCATCTACATGAGCCAGAGAGCCCGTGCAGCTGCCCGGTACTACTAGTGGACACCAAG 594
Db 535 TCCCATCTACATGAGCCAGAGAGCCCGTGCAGCTGCCCGGTACTACTAGTGGACACCAAG 594
QY 541 ACTTTTACAGACAAAGAAACCGGTGACGATGCCACCAACCATGTGTGGAAACATCGC 600
Db 541 ACTTTTACAGACAAAGAAACCGGTGACGATGCCACCAACCATGTGTGGAAACATCGC 600
QY 595 CTGACATCACTCCCAACAGAGACTACACCATGTGAGCAGTACAGCGCACCG 652
Db 595 CTGACATCACTCCCAACAGAGACTACACCATGTGAGCAGTACAGCGCACCG 652
QY 601 ATTGAGAGGACCGACCTTGAACAAAGTGGCAACAGTTCACTGACGAGGACCGCTG 658
Db 601 ATTGAGAGGACCGACCTTGAACAAAGTGGCAACAGTTCACTGACGAGGACCGCTG 658

RESULT 8
US-09-277-716-30
; Sequence 30, Application US/0927716A
; Patent No. 6232107
; GENERAL INFORMATION:
; APPLICANT: Bryan, Bruce
; APPLICANT: Szent-Gyorgyi, Christopher
; APPLICANT: PROLUME, LTD.
; TITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE
; CURRENT APPLICATION NUMBER: US/09/277,716A
; EARLIER FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: 60/102,939
; EARLIER FILING DATE: 1998-10-01
; EARLIER APPLICATION NUMBER: 60/089,367
; EARLIER FILING DATE: 1998-06-15
; EARLIER APPLICATION NUMBER: 60/079,624
; EARLIER FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 1104
; TYPE: DNA
; ORGANISM: Ptilosarcus gurneyi
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (34)..(747)
; FEATURE:
; OTHER INFORMATION: Ptilosarcus Green Fluorescent Protein (GFP) (Insert A)
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US-09-277-716-30
Query Match 17.6%; Score 119; DB 3; Length 1104;
Best Local Similarity 49.4%; Pred. No. 1.7e-15;
Matches 308; Conservative 0; Mismatches 315; Indels 0; Gaps 0;

QY 23 TCACGAGTTCATGCGCTTCAAGGTGCGCATGAGAGGCAACCGTGAACGCGCAAGTTCG 82
Db 23 TCACGAGTTCATGCGCTTCAAGGTGCGCATGAGAGGCAACCGTGAACGCGCAAGTTCG 82
QY 65 TGAAGAGATTAATGTGCGCAAGAGCTAGCGTGAAGAAATGATGAACATTCAGTTT 124
Db 65 TGAAGAGATTAATGTGCGCAAGAGCTAGCGTGAAGAAATGATGAACATTCAGTTT 124
QY 83 AGATCAGAGGCGAGGCGAGGCGCGCCCTTACGAGGCGCACACACCGTGAAGTTGAAG 142
Db 83 AGATCAGAGGCGAGGCGAGGCGCGCCCTTACGAGGCGCACACACCGTGAAGTTGAAG 142
QY 125 CCATGAGAGAAATTTGAGAAAGCATATGATTTATTTGAAACCAATGATGAAATCCGG 184
Db 125 CCATGAGAGAAATTTGAGAAAGCATATGATTTATTTGAAACCAATGATGAAATCCGG 184
QY 143 TGACCAAGGCGGCGCCCTGCGCTTGGGGAATCTGTGCCCCCAATTCAGTACG 202
Db 143 TGACCAAGGCGGCGCCCTGCGCTTGGGGAATCTGTGCCCCCAATTCAGTACG 202
QY 185 TTACAAAGGAGAGTCCGTGTCATTCGCTTCAATTTGTTTCCATGCTTCCAAATACG 244
Db 185 TTACAAAGGAGAGTCCGTGTCATTCGCTTCAATTTGTTTCCATGCTTCCAAATACG 244
QY 203 GCTCAAGGTGATGAGAGACCCCGCGCATCCCGACTCAAGAAAGCTGCTTCC 262
Db 203 GCTCAAGGTGATGAGAGACCCCGCGCATCCCGACTCAAGAAAGCTGCTTCC 262
QY 245 GGAATCGACTTTCAGAAATACCAAGACGATGCGACTACTTTGTTCAATCATTC 304
Db 245 GGAATCGACTTTCAGAAATACCAAGACGATGCGACTACTTTGTTCAATCATTC 304
QY 263 CCGAGGCTTCAAGTGGAGCGCGTGAATGAATTCGAGAGACGCGCGTGGACCGTGA 322
Db 263 CCGAGGCTTCAAGTGGAGCGCGTGAATGAATTCGAGAGACGCGCGTGGACCGTGA 322
QY 305 CGGCTGATTTTTCACGAAAGAAATCTACGCTTTGAAGATGGCCCATTTGTCATTC 364
Db 305 CGGCTGATTTTTCACGAAAGAAATCTACGCTTTGAAGATGGCCCATTTGTCATTC 364
QY 323 CCCAGACTCTCTCTGACAGAGCGGCTCTTCAATCAAGGTGAAGTTTATCGCGTGA 382
Db 323 CCCAGACTCTCTCTGACAGAGCGGCTCTTCAATCAAGGTGAAGTTTATCGCGTGA 382
QY 365 GTTCAGATTAATGATTGAAGATGATTAAGTTTCACTACAAAGTGAATGAGGCAACG 424
Db 365 GTTCAGATTAATGATTGAAGATGATTAAGTTTCACTACAAAGTGAATGAGGCAACG 424
QY 383 ACTTCCCTCCGAGGCGCGCGTGAAGAGAAACCATGGGCGTGGAGGCGCTCACCG 442
Db 383 ACTTCCCTCCGAGGCGCGCGTGAAGAGAAACCATGGGCGTGGAGGCGCTCACCG 442
QY 425 GTTTCCTAGTACGAGCCCGTGAATGCAAAAACCATCTTGGCATGAGAGCCATGTTTG 484
Db 425 GTTTCCTAGTACGAGCCCGTGAATGCAAAAACCATCTTGGCATGAGAGCCATGTTTG 484
QY 443 AGCGCTGTACCCCGCGAGCGCGTGAAGGCGAGATCCACAGGCGCTGAAGCTGA 502
Db 443 AGCGCTGTACCCCGCGAGCGCGTGAAGGCGAGATCCACAGGCGCTGAAGCTGA 502
QY 485 AGGTGTCTCATATGAACAGCGCGTCTGTGGGAGAGTGAATCGTTTACAAATTCG 544
Db 485 AGGTGTCTCATATGAACAGCGCGTCTGTGGGAGAGTGAATCGTTTACAAATTCG 544
QY 503 AGGACGCGGCGCATCACTGCTGTGATTCATAGTCAATCAATGAGGCAAGAGCCCGTGC 562
Db 503 AGGACGCGGCGCATCACTGCTGTGATTCATAGTCAATCAATGAGGCAAGAGCCCGTGC 562
QY 545 AGTCAGGAGAACTATTACTGTGCGCACATGAAGAAACCTTTTACAGATCCAAAGGTGAGTGA 604
Db 545 AGTCAGGAGAACTATTACTGTGCGCACATGAAGAAACCTTTTACAGATCCAAAGGTGAGTGA 604
QY 563 AGTCCCGCGGCTACTACTACGAGGACCAAGCTGGAATCACTCCCAACAGAGACT 622
Db 563 AGTCCCGCGGCTACTACTACGAGGACCAAGCTGGAATCACTCCCAACAGAGACT 622
QY 605 AAGAAATTCGGAATATCACTTATTCATTCGTCTGAGAAACCTTACGTGGAAGAG 664
Db 605 AAGAAATTCGGAATATCACTTATTCATTCGTCTGAGAAACCTTACGTGGAAGAG 664
QY 623 ACACCATGTGAGAGCATGAGAG 645
Db 623 ACACCATGTGAGAGCATGAGAG 645
QY 665 GAACTTGTGGAACACACGAG 687
Db 665 GAACTTGTGGAACACACGAG 687

RESULT 9
US-09-609-161B-30
; Sequence 30, Application US/09609161B
; Patent No. 6436682
; GENERAL INFORMATION:
; APPLICANT: Bryan, Bruce
; APPLICANT: Szent-Gyorgyi, Christopher
; APPLICANT: PROLUME, LTD.
; TITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE LUC
; CURRENT APPLICATION NUMBER: US/09/609,161B
; EARLIER FILING DATE: 2000-06-30
; EARLIER APPLICATION NUMBER: 09/277,716
; EARLIER FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: 60/102,939
; EARLIER FILING DATE: 1998-10-01
; EARLIER APPLICATION NUMBER: 60/089,367
; EARLIER FILING DATE: 1998-06-15
; EARLIER APPLICATION NUMBER: 60/079,624
; EARLIER FILING DATE: 1998-03-27
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; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 1104
; TYPE: DNA
; ORGANISM: *Ptiliosarcus gurneyi*
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (34)..(747)
; OTHER INFORMATION: *Ptiliosarcus Green Fluorescent Protein (GFP) (insert A)*
US-09-161B-30

Query Match 17.6%; Score 119; DB 3; Length 1104;
Best Local Similarity 49.4%; Pred. No. 1.7e-15;
Matches 308; Conservative 0; Mismatches 315; Indels 0; Gaps 0;

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QY 23 TCACCGAGTTGATGCGCTTCAAGTGGCATGAGAGGCACTGTGAACGCCCAAGATTCC 82
DB 65 TGAAGAGATTATGTGCGCAAAAGCTAGCGTTGAAGAGATCGTGAACATCACGTTT 124
QY 83 AGATCGAGGCGAGGCGCGCCCTACGAGGCGCAACAACCGTGAAGTTGAAG 142
DB 125 CCAATGAGAGATTGGAAGAGCAATGATATTGGAACCAATGATGCAATCCGG 184
QY 143 TGACCAAGGCGCGCCCTGCGCTTGCCTGGGACATCTGTCCGCCAGTTCCAGTAC 202
DB 185 TTAACAAGGAGGATCGCTTGCATTTGCGATATTGTTCCATAGCTTTCCAAATAC 244
QY 203 GCTCCAGGTGATGTAAGACACCCCGGACATCCCGACTCAAGAAAGCTGTCTCC 262
DB 245 GGAATCGCATTTTACGAAATACCAAGACGACATTCGCACTTCTTTCAATCATTC 304
QY 263 CCGAGGCTTCAAGTGGAGCGCGGTGATGAACCTTGAAGACGCGCGCGACCGTGA 322
DB 305 CGGCTGATTTTCTACGAAAGAAATCTACGCTTTGAAGATGGCGCATTTGACATTC 364
QY 323 CCGAGACTCTCTCCCTGAGAGACGCGCTTCACTCAAGATGAAGTTCACTGCGGTGA 382
DB 365 GTTCAGATATTAAGTTAGAAATGATGATTAAGTTCCACTCAAAAGTGAATGAGCAAC 424
QY 383 ACTTCCCTCCGAGCGCCCGGTGATGCAAGAAAGACATGGGCTGGAGGCTTCCACCG 442
DB 425 GTTTCCTTAAGTACGAGACCGGTGATGCAAAAGCCATCTCGGATGAGGCACTGTTG 484
QY 443 AGCGCTGTACCCCGGAGCGCGGTGTAAGGCGAGATCCACAAGGCCCTGAAGCTGA 502
DB 485 AGGTGCTATCATGAACAGCGCGCTTGTGTGGGAGAGTAACTCTGTTTACAACTCG 544
QY 503 AGACGCGGCGCACTACCTGTGTGAGTTCAAGTCACTACATGCGCAAGAGCCCGTGC 562
DB 545 AGTCAAGGAATTAATTAATCTGTGCAATGAAGAAAGTTTACAGATCCAAAGTGAAGTGA 604
QY 563 AGCTGCCGCTACTACTACGTGAGCAACCAAGCTGAGCATCACTCCCAACAAGAGACT 622
DB 605 AAGAAATTCGGAATATCACTTATTCATCTGTGAGAGAAACCTACGTGAAGAG 664
QY 623 ACACCATGTGAGAGCAAGTACGAG 645
DB 665 GAAGCTTGTGGAACAACACGAG 687
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RESULT 10
US-09-277-716-31
; Sequence 31, Application US/09277716A
; Patent No. 6232107
; GENERAL INFORMATION:
; APPLICANT: Bryan, Bruce
; APPLICANT: Szent-Gyorgyi, Christopher
; APPLICANT: PROLUME, LTD.
; TITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE
; CURRENT FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: 60/102,939

; EARLIER FILING DATE: 1998-10-01
; EARLIER APPLICATION NUMBER: 60/089,367
; EARLIER FILING DATE: 1998-06-15
; EARLIER APPLICATION NUMBER: 60/079,624
; EARLIER FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 1279
; TYPE: DNA
; ORGANISM: *Ptiliosarcus gurneyi*
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(720)
; OTHER INFORMATION: *Ptiliosarcus Green Fluorescent Protein (GFP) (insert B)*
US-09-277-716-31

Query Match 17.6%; Score 119; DB 3; Length 1279;
Best Local Similarity 49.4%; Pred. No. 1.7e-15;
Matches 308; Conservative 0; Mismatches 315; Indels 0; Gaps 0;

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QY 23 TCACCGAGTTGATGCGCTTCAAGTGGCATGAGAGGCACTGTGAACGCCCAAGATTCC 82
DB 38 TGAAGAGATTATGTGCGCAAAAGCTAGCGTTGAAGAGATCGTGAACATCACGTTT 97
QY 83 AGATCGAGGCGAGGCGCGCCCTACGAGGCGCAACAACCGTGAAGTTGAAG 142
DB 98 CCAATGAGAGATTGGAAGAGCAATGATATTGGAACCAATGATGCAATCCGG 157
QY 143 TGACCAAGGCGCGCCCTGCGCTTGCCTGGGACATCTGTCCGCCAGTTCCAGTAC 202
DB 158 TTAACAAGGAGGATCGCTTGCATTTGCGATATTGTTCCATAGCTTTCCAAATAC 217
QY 203 GCTCCAGGTGATGTAAGACACCCCGGACATCCCGACTCAAGAAAGCTGTCTCC 262
DB 218 GGAATCGCATTTTACGAAATACCAAGACGACATTCGCACTTCTTTCAATCATTC 277
QY 263 CCGAGGCTTCAAGTGGAGCGCGGTGATGAACCTTGAAGACGCGCGCGACCGTGA 322
DB 278 CGGCTGATTTTCTACGAAAGAAATCTACGCTTTGAAGATGGCGCATTTGACATTC 337
QY 323 CCGAGACTCTCTCCCTGAGAGACGCGCTTCACTCAAGATGAAGTTCACTGCGGTGA 382
DB 338 GTTCAGATATTAAGTTAGAAATGATGATTAAGTTCCACTCAAAAGTGAATGAGCAAC 397
QY 383 ACTTCCCTCCGAGCGCCCGGTGATGCAAGAAAGACATGGGCTGGAGGCTTCCACCG 442
DB 398 GTTTCCTTAAGTACGAGACCGGTGATGCAAAAGCCATCTCGGATGAGGCACTGTTG 457
QY 443 AGCGCTGTACCCCGGAGCGCGGTGTAAGGCGAGATCCACAAGGCCCTGAAGCTGA 502
DB 458 AGGTGCTATCATGAACAGCGCGCTTGTGTGGGAGAGTAACTCTGTTTACAACTCG 517
QY 503 AGACGCGGCGCACTACCTGTGTGAGTTCAAGTCACTACATGCGCAAGAGCCCGTGC 562
DB 518 AGTCAAGGAATTAATTAATCTGTGCAATGAAGAAAGTTTACAGATCCAAAGTGAAGTGA 577
QY 563 AGCTGCCGCTACTACTACGTGAGCAACCAAGCTGAGCATCACTCCCAACAAGAGACT 622
DB 578 AAGAAATTCGGAATATCACTTATTCATCTGTGAGAGAAACCTACGTGAAGAG 637
QY 623 ACACCATGTGAGAGCAAGTACGAG 645
DB 638 GAAGCTTGTGGAACAACACGAG 660
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RESULT 11
US-09-609-161B-31
; Sequence 31, Application US/09609161B
; Patent No. 643682
; GENERAL INFORMATION:
; APPLICANT: Bryan, Bruce

APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: PROLUME, LTD.
TITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE LUC
AND FLUORESCENT PROTEINS AND THE USE THEREOF IN DIAGNOSTICS, HIGH
TITLE OF INVENTION: SCREENING AND NOVELTY ITEMS
FILE REFERENCE: 24729-121B
CURRENT APPLICATION NUMBER: US/09/609,161B
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/277,716
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 60/102,939
PRIOR FILING DATE: 1998-10-01
PRIOR APPLICATION NUMBER: 60/089,367
PRIOR FILING DATE: 1998-06-15
PRIOR APPLICATION NUMBER: 60/079,624
PRIOR FILING DATE: 1998-03-27
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 31
LENGTH: 1279
TYPE: DNA
ORGANISM: *Ptilosarcus gurneyi*
FEATURE:
NAME/KEY: CDS
LOCATION: (7)..(720)
OTHER INFORMATION: *Ptilosarcus Green Fluorescent Protein (GFP) (Insert B)*
US-09-609-161B-31

Query Match 17.6%; Score 119; DB 3; Length 1279;
Best Local Similarity 49.4%; Pred. No. 1.7e-15;

Matches 308; Conservative 0; Mismatches 315; Indels 0; Gaps 0;

QY 23 TCACGAGTTCATGCGCTTCAAGAGTGGCGATGAGGGCACCCTGAACGGCCACGAGTTCCG 82
DB 38 TGAAGAGATTAATGTCGCGCAAAAGCTAGCGTTGAAGATCGTGAACATCAGTTTTTT 97
QY 83 AGATGAGGGGAGGGGCGAGGCGCGCCCTACGAGGGCCCAACACCGTGAAGTTGAAG 142
DB 98 CCATGAGAGATTTGGAAAGGCAATGTAATTTTGAAGAACCAATTGATGCAATCCGGG 157
QY 143 TGACCAAGGGCGGCGCCCTGCGCTTCCGCTGGAGACATCTGTCGCCCGCCAGTTCAGATAG 202
DB 158 TTACAAAGGAGAGTCCGTTGCCATTCGCTTGAATGTTTCCATAGCTTTCCATAGC 217
QY 203 GCTCAAGGTGATGCTGAAGCAACCCCGCGACATCCCGCATCAAGAAAGCTGCTTCC 262
DB 218 GGAATCGCACTTTCAGAAATACCAAGACGACATTCGCGCATCTTGTTCATCATTTTC 277
QY 263 CCGAGGGCTTCAAGTGGAGCGCGGTGATGAATTCGAGAGACGGCGCGGTGGAGACGTGA 322
DB 278 CGGCTGATTTTCTACGAAAGAAATCTAGCGCTTGAAGATGGCGCATTTGTGAATTC 337
QY 333 CCCAGACTCTCCCTGCGAGACGGCGTGTTCATCTACAGAGTGAAGTTCAATCGCGTGA 382
DB 338 GTTCAGATTAATAGTTTGAAGATGAATTAAGTTCCATCAAAAGTGAAGTGAAGCAAG 397
QY 383 ACTTCCTCCGCGAGCGCGCGGTGATGCAAGAGAACATGCGGTGGAGAGCGCTTCACCG 442
DB 398 GTTTCCTTAATAGTGAAGCGCGGTGATGCAAAAGCAATCTCGGCTATGAGCATGTTG 457
QY 443 AGCGCTGATACCCCGCGAGCGCGGTGATGAAGGGGAGATTCACAAAGCGCTGAAGCTGA 502
DB 458 AGTGGTCTACATGAACAGCGCGGTGATGAGAGAGTGAATCTCGTTTACAAATTCG 517
QY 503 AGGAGCGGCGCCATCACTGATGAGTTCAAGTTCATCTACATGCGCAAGAGCCCGTGC 562
DB 518 AGTCAAGGGAATTAATCTGTCGCCATGAAAGCGTTTACAGATCCAAAGGTGAGTGA 577
QY 563 AGCTCCCGGCTACTACTGATGAGACCAAGCTGACATCCTTCCCAAGAGAGACT 622
DB 578 AAGAAATCCCGGAAATATCACTTATCATCATCATCTGAGAGAAACCTAAGTGAAGAG 637
QY 623 AACACATGATGAGAGATGAGAG 645

DB 638 GAGCTTCGTGGACACACAG 660

RESULT 12
US-09-459-956-4

Sequence 4, Application US/09459956
Patent No. 6342379

GENERAL INFORMATION:
APPLICANT: Tsien, Roger Y.

APPLICANT: Gonzalez, III, Jesus E.
TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY
TITLE OF INVENTION: OPTICAL METHODS

FILE REFERENCE: REGEM1290-4
CURRENT APPLICATION NUMBER: US/09/459,956
CURRENT FILING DATE: 1999-12-13

PRIOR APPLICATION NUMBER: 08/765,860
PRIOR FILING DATE: 1999-05-08

PRIOR APPLICATION NUMBER: 08/481,977
PRIOR FILING DATE: 1995-06-07

PRIOR APPLICATION NUMBER: PCT/US96/09652
PRIOR FILING DATE: 1996-06-06

NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 4
LENGTH: 696

TYPE: DNA
ORGANISM: *Zoanthus sp*

US-09-459-956-4

Query Match 16.3%; Score 110.4; DB 3; Length 696;
Best Local Similarity 52.5%; Pred. No. 9.1e-14;
Matches 296; Conservative 0; Mismatches 256; Indels 12; Gaps 2;

QY 1 ATGCGCTCTCCGAGACGTATCAACCGATTCATGCGCTTCAAGTGGCGATGAGAGGC 60
DB 1 ATGGCTATTCAAGACAGCTCTAAGAAAGAAATGACATGAAATACACATGAGAGG 60
QY 61 ACCGTGAAGCGCCACGAGTTGAGATGAGGGCGGAGGGCGCGCCCTTACAGAGGC 120
DB 61 TGCGTCAACGAGACATTAATTTGTGTATCGGGCGAGGCGCATTTGATTCGTTCAAGGG 120
QY 121 CACAACACCGGAAGTTGAAGTGAACAGGGGCGCGCCCTGCGCTGGCGGAGCATC 180
DB 121 AAACGACTATTATCTGTGTATGAGAGAGAGAGATTTTCACTGAATATCTCAAGACATGA 180
QY 181 CTGTCCCGCCAGTTCCAGTACAGGCTCAAGGTATGATGAGACACCCGCGACATCCCG 240
DB 181 TTGTAGTGGCTTAAATAGGAGACAGAGATTTTCACTGAATATCTCAAGACATGA 240
QY 241 GACTTCAAGAAAGCTGTCTTCCCGAGGGCTTCAAGTGGAGAGCGGTATGAATTTCCAG 300
DB 241 GACTTCAAGAAAGCTGTCTTCCCGAGGGCTTCAAGTGGAGAGCGGTATGAATTTCCAG 300
QY 301 GAGCGCGCGGAGGAGCGCGTACACCGAGATCTCTCCG-----CAGAGCGGCTTCC 354
DB 301 GATGAGAGAGTGTGATATGAGATGATATTAAGTGAAGTGTCAAGAGAAATCTGCAAT 360
QY 355 ATCTCAAGATGAGATGATGAGCGCTGAACTTCCCTCCGACGCGCGCGTATGAGAG 414
DB 361 TATATTAAGACATATTTAATGAGATGAATTTTCTGTGATGAGACCTGTATGAGAAAG 420
QY 415 AAGACATAGGCTGGAGAGCGCTCCACGAG-----CGCTGTACCCCGGAGCGCGT 468
DB 421 ATGACATTAATCTGGAAGATCTCTGCGAGAAATCATGACATGATCTTAAGCAGGAGTA 480
QY 469 CTGAAGGCGGAGATCAAGAGCGCTGAAGTGAAGAGCGGCGGCACTACTGTGAG 528
DB 481 CTGAAGGAGATGTCTCATGATCTCTTGTGAAGATGTGTGGCGCTTACCGGTGCGAG 540
QY 529 TTCAATCATCTACATGAGCAAG 552
DB 541 TTGACACAGTTTACAAAGCAAG 564

Db 361 TATCATGATGTCATTTTATGAGTGAATTTCTCGTGAATGAGACTGTGATGAAAAAG 420
QY 415 AAGACCATGGGCTGGAGAGCCTTCAACCGAG-----CGCTGTACCCCGCAGCGGCTG 468
Db 421 ATGACAGATTAATCTGGAGAGCATCTCGCGAGATCATATACAGTACTTAAGCAGGGGATA 480
QY 469 CTGAAGGGGAGATCCACAAGGCCCTGAAGCTGAAGAGACGGCGCACTACTGTGTGAG 528
Db 481 TTGAAGGGGAGTGTCTTCATGTACTCTTCTGAAGAGTGTGGGGTTTACGGTCCAA 540
QY 529 TTCAAGTCCATCTACATGAGCCCAAG 552
Db 541 TTCGACACAGTTTACAAAGCAAAAG 564

RESULT 15
US-09-486-241-31

; Sequence 31, Application US/09486241
; Patent No. 6472184
; GENERAL INFORMATION:
; APPLICANT: Hegemann, Peter
; TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEIC ACID
; TITLE OF INVENTION: POLYMERS
; FILE REFERENCE: 3910/06706
; CURRENT APPLICATION NUMBER: US/09/486,241
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: PCT/EP98/05219
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: DE19736591.4
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 31
; LENGTH: 717
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Modified gene from Aquorea victoria
US-09-486-241-31

Query Match 14.6%; Score 99; DB 4; Length 717;
Best Local Similarity 51.0%; Pred. No. 1.9e-11;
Matches 327; Conservative 0; Mismatches 290; Indels 24; Gaps 3;

QY 1 ATGCGCTCTCCGAGAACGTCATCAACCGAGTTCAATCGCTTCAAGGTGCGCATGAGAGGC 60
Db 1 ATGTCACAGGGGAGAGAGCTGTTCAACGGGTGTGTCCTCCATCTGTGAGACTGAGACGAC 60
QY 61 ACCGTGAACGGGCAAGAGTTGAGATCGAGGGCGAGGGGCGGCCGCCCTACAGAGGC 120
Db 61 GACGTGAACGGGCAAGAGTTCTCCGTCTCCGGCGAGGGGTGAGCGCCACCTACGAGC 120
QY 121 CACAACACCGTGAAGTTGAAGGTGACCAAGGGCGGCCCTGCTGCTGAGACATC 180
Db 121 AAGGTGACCTGTAAATTCATCTGACCA---CCGGCAAGCTGCCGTGCCCTGAGCCACC 177
QY 181 CTGTCCCCCAGTTCCAGTACGGCTCCAAAGGTGAAGTGAAGCACCCTGCGACAT--- 236
Db 178 CTGTCAACCACTTCACTACAGTGTGAGTGTCTTCCCGCTACCCGACCACTATGAAG 237
QY 237 ---CCCGACTCAAGAGCTGTCTTCCCGAGGGCTTCAAGTGGAGCGGTGATGAAC 294
Db 238 CAGCAGAGCTTTTCAAGTCCCGCAGTCCCGAGGGCTAGTCAAGAGGACACATCTTC 297
QY 295 TTTCAGAGCGGCGGCTGCGACCGTGAACCCAGACTCTCCCTGACAGACGGCTGCTTC 354
Db 298 TTCAAGAGAGAGGAGCACTACAAAGACCGCGCGAGGTCAAGTGAAGGGGAGACCTCG 357
QY 355 ATCTCAAGGTGAAGTTCAATCGGCTGAATCTTCCCTCCAGAGGCGCCGTGATGCAAG 414
Db 358 GTGAACCCGATCGAGCTGAAGGGCATTCGCTTCAAGAGAGACGGCAACATCTGTGGCCAC 417

QY 415 AAGACCATGGGCTGGAGAGCCTTCAACCGAGCGCTGTATCCCGCGAGCGGCTGTGAAG 474
Db 418 AAGCTGAGGTACACTTCACTCCCAACAGGTGATCATATGCGCCGACAGAGAAAGAC 477
QY 475 GCGGATCCACAAAGGCCCTGAAGTGAAGACGGCGGCACCTACTGCTGAGATT--- 530
Db 478 GGCATCAAGGTGAATTCAGAGTCCGCCAACAATCGAGAGACGGCTCCGTGCACTGGCC 537
QY 531 -----CAGTCAATCTACATGAGCCCAAGAAAGCCCGTCACTGCTCCGCTACTAC 579
Db 538 GACCACTACACAGCAACACCCCATCGCGATGCGCCCGTCTGCTGCGCAACACAC 597
QY 580 TACGTGACACCAAGCTGAGATCACTCTCCCAACAGAGGA 620
Db 598 TACTGTCCACCAAGTCCGCTGTCTCAAGAGACCCCAACGA 638

Search completed: May 29, 2005, 21:17:18
Job time : 158.23 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 29, 2005, 21:06:21 ; Search time 545.658 Seconds

(without alignments)
7628.632 Million cell updates/sec

Title: US-10-081-864a-14

Perfect score: 678
Sequence: 1 atggcctccctccgagaacgt.....gccaccactgtctctgtaa 678Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5700845 seqs, 3069779757 residues

Total number of hits satisfying chosen parameters: 11401690

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA.*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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10: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
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12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
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15: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
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17: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US10F_NEW_PUB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	678	100.0	678	US-10-006-922-36	Sequence 36, Appl
2	678	100.0	678	US-10-081-864-14	Sequence 14, Appl
3	676.4	99.8	678	US-10-315-920-5	Sequence 5, Appl
4	672.2	99.1	1050	US-10-060-857-7	Sequence 7, Appl
5	670.6	98.9	7495	US-10-742-828-5	Sequence 5, Appl
6	670.2	98.8	675	US-10-006-922-38	Sequence 38, Appl
7	670.2	98.8	675	US-10-081-864-13	Sequence 13, Appl
8	670.2	98.8	747	US-10-785-862-10	Sequence 10, Appl
9	668.4	98.3	678	US-10-315-920-3	Sequence 3, Appl
10	666.4	98.3	7508	US-10-742-828-4	Sequence 4, Appl
11	665.2	98.1	678	US-10-081-864-7	Sequence 7, Appl

12	665.2	98.1	678	US-10-315-920-1	Sequence 1, Appl
13	661.6	97.6	681	US-10-121-258-3	Sequence 3, Appl
14	661.6	97.6	681	US-10-121-258-23	Sequence 23, Appl
15	661.6	97.6	4692	US-10-161-403-29	Sequence 29, Appl
16	661.6	97.6	4692	US-10-433-640-16	Sequence 16, Appl
17	661.6	97.6	6984	US-10-001-189-45	Sequence 45, Appl
18	661.6	97.6	7910	US-10-169-050-20	Sequence 20, Appl
19	661.6	97.6	9320	US-10-471-065-20	Sequence 20, Appl
20	661.6	97.6	9658	US-10-609-019-4	Sequence 4, Appl
21	661.6	97.6	9678	US-10-609-019-3	Sequence 3, Appl
22	661.6	97.6	10263	US-10-609-019-2	Sequence 2, Appl
23	660	97.3	681	US-10-006-922-35	Sequence 35, Appl
24	660	97.3	681	US-10-006-922-37	Sequence 37, Appl
25	660	97.3	5436	US-10-169-050-46	Sequence 46, Appl
26	659.6	97.3	1638	US-10-214-932-51	Sequence 51, Appl
27	659.6	97.3	1647	US-10-214-932-75	Sequence 75, Appl
28	655.2	96.6	723	US-10-152-296-1	Sequence 1, Appl
29	655.2	96.6	723	US-10-739-656-1	Sequence 1, Appl
30	649.8	95.8	678	US-10-121-258-5	Sequence 5, Appl
31	629.6	92.9	681	US-10-121-258-7	Sequence 7, Appl
32	614.2	90.6	681	US-10-311-030-8	Sequence 8, Appl
33	614.2	90.6	713	US-10-311-030-11	Sequence 11, Appl
34	614.2	90.6	713	US-10-311-030-12	Sequence 12, Appl
35	568.6	83.9	675	US-10-724-178-15	Sequence 15, Appl
36	568.6	83.9	678	US-10-121-258-9	Sequence 9, Appl
37	556.4	82.1	678	US-10-006-922-43	Sequence 43, Appl
38	556.4	82.1	678	US-10-081-864-11	Sequence 11, Appl
39	470.6	69.4	549	US-10-724-178-1040	Sequence 1040, Ap
40	459	67.7	501	US-10-724-178-1022	Sequence 1022, Ap
41	438.4	64.7	564	US-10-724-178-1036	Sequence 1036, Ap
42	438	64.6	678	US-09-967-772-6	Sequence 6, Appl
43	438	64.6	678	US-10-006-922-11	Sequence 11, Appl
44	438	64.6	678	US-10-121-258-2	Sequence 2, Appl
45	438	64.6	678	US-10-132-067-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-10-006-922-36
; Sequence 36, Application US/10006922
; Publication No. US20020197676A1
; GENERAL INFORMATION:
; APPLICANT: Lukyanov, Sergey A
; APPLICANT: Fradkov, Arcady F.
; APPLICANT: Labas, Yulii A.
; APPLICANT: Matz, Mikhail V.
; APPLICANT: Terakikh, Alexey
; TITLE OF INVENTION: No. US20020197676A1 Chromophores/Fluorophores and
; FILE REFERENCE: CLON-035CIP
; CURRENT FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: US/10/006,922
; PRIOR APPLICATION NUMBER: 09/120,330
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: 09/457,898
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 09/458,144
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 09/458,477
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 09/457,556
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 09/444,338
; PRIOR FILING DATE: 1999-11-19
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 678
; TYPE: DNA
; ORGANISM: Discosoma species
; US-10-006-922-36

Query March 100.0%; Score 678; DB 13; Length 678;
Best Local Similarity 100.0%; Pred. No. 2e-167;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ATGGCTCTCTCCGAGAACGTCATCAACGAGTTTCATGCGCTTCAAGTCCGATGAGAGGC 60
QY 61 ACCGTGAACCGCCACGAGTTCAGATTCAGAGCGAGCGAGCGCGCCCTTACGAGGC 120
DB 61 ACCGTGAACCGCCACGAGTTCAGATTCAGAGCGAGCGAGCGCGCCCTTACGAGGC 120
QY 121 CACAACACCGTGAAGTTGAAGGTGACCAAGGGCGCGCCCTTGCCTTGGCGTGGGACATC 180
DB 121 CACAACACCGTGAAGTTGAAGGTGACCAAGGGCGCGCCCTTGCCTTGGCGTGGGACATC 180
QY 181 CTGTCCCCCAAGTTCCAGTACGGCTCAAGGTGTACGTGAAGCACCCCGCGACATCCCC 240
DB 181 CTGTCCCCCAAGTTCCAGTACGGCTCAAGGTGTACGTGAAGCACCCCGCGACATCCCC 240
QY 241 GACTACAAAGAACTGTCTTCTCCGAGGCTTCAAGTGGAGCGGTGATGAATTCGAG 300
DB 241 GACTACAAAGAACTGTCTTCTCCGAGGCTTCAAGTGGAGCGGTGATGAATTCGAG 300
QY 301 GACGCGCGCGTGGGACCGGTGACCCAGGACTCTCTCCGAGGACGCGCTTCAATCTAC 360
DB 301 GACGCGCGCGTGGGACCGGTGACCCAGGACTCTCTCCGAGGACGCGCTTCAATCTAC 360
QY 361 AAGGTGAAGTTCAATCGGCGTGAATCTCCCTCCGAGCGCCCGGTGATGACAGAGAAC 420
DB 361 AAGGTGAAGTTCAATCGGCGTGAATCTCCCTCCGAGCGCCCGGTGATGACAGAGAAC 420
QY 421 ATGGCTGGGAGGCTTCCACGAGCGCTGTACCCCGCGAGCGGTGTCTGAAGGGCGAG 480
DB 421 ATGGCTGGGAGGCTTCCACGAGCGCTGTACCCCGCGAGCGGTGTCTGAAGGGCGAG 480
QY 481 ATCCACAAGGCTCTGAAGCTGAAGGACGCGCGGACCTACCTGTTGAGTTCAAGTCCATC 540
DB 481 ATCCACAAGGCTCTGAAGCTGAAGGACGCGCGGACCTACCTGTTGAGTTCAAGTCCATC 540
QY 541 TACATGGCCAAAGAACCCGTGCAAGCTGCGCGCTTACTACTGTTGAGTCAAGCTGAGC 600
DB 541 TACATGGCCAAAGAACCCGTGCAAGCTGCGCGCTTACTACTGTTGAGTCAAGCTGAGC 600
QY 601 ATCACTCTCCCAACAAGGACTGACCACTGCTGAGGACGTTGAGTCAAGCTGAGC 660
DB 601 ATCACTCTCCCAACAAGGACTGACCACTGCTGAGGACGTTGAGTCAAGCTGAGC 660
QY 661 CACCACTGTTCTCTGTAA 678
DB 661 CACCACTGTTCTCTGTAA 678
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RESULT 2

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US-10-081-864-14
; Sequence 14, Application US/10081864
; Publication No. US20030022287A1
; GENERAL INFORMATION:
; APPLICANT: Lukyanov, Sergey
; APPLICANT: Lukyanov, Konstantin
; APPLICANT: Yamshevich, Yuriy
; APPLICANT: Savitsky, Alexander
; APPLICANT: Pradkov, Arcady
; TITLE OF INVENTION: No. US20030022287A1 Aggregating Fluorescent Proteins and
; FILE REFERENCE: CLON-067
; CURRENT APPLICATION NUMBER: US/10/081, 864
; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: 10/006, 922
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/270, 983
; PRIOR FILING DATE: 2001-02-21
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NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 678
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: non-aggregating mutant
US-10-081-864-14

Query March 100.0%; Score 678; DB 14; Length 678;
Best Local Similarity 100.0%; Pred. No. 2e-167;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGGCTCTCTCCGAGAACGTCATCAACGAGTTTCATGCGCTTCAAGTCCGATGAGAGGC 60
DB 1 ATGGCTCTCTCCGAGAACGTCATCAACGAGTTTCATGCGCTTCAAGTCCGATGAGAGGC 60
QY 61 ACCGTGAACCGCCACGAGTTCAGATTCAGAGCGAGCGAGCGCGCCCTTACGAGGC 120
DB 61 ACCGTGAACCGCCACGAGTTCAGATTCAGAGCGAGCGAGCGCGCCCTTACGAGGC 120
QY 121 CACAACACCGTGAAGTTGAAGGTGACCAAGGGCGCGCCCTTGCCTTGGCGTGGGACATC 180
DB 121 CACAACACCGTGAAGTTGAAGGTGACCAAGGGCGCGCCCTTGCCTTGGCGTGGGACATC 180
QY 181 CTGTCCCCCAAGTTCCAGTACGGCTCAAGGTGTACGTGAAGCACCCCGCGACATCCCC 240
DB 181 CTGTCCCCCAAGTTCCAGTACGGCTCAAGGTGTACGTGAAGCACCCCGCGACATCCCC 240
QY 241 GACTACAAAGAACTGTCTTCTCCGAGGCTTCAAGTGGAGCGGTGATGAATTCGAG 300
DB 241 GACTACAAAGAACTGTCTTCTCCGAGGCTTCAAGTGGAGCGGTGATGAATTCGAG 300
QY 301 GACGCGCGCGTGGGACCGGTGACCCAGGACTCTCTCCGAGGACGCGCTTCAATCTAC 360
DB 301 GACGCGCGCGTGGGACCGGTGACCCAGGACTCTCTCCGAGGACGCGCTTCAATCTAC 360
QY 361 AAGGTGAAGTTCAATCGGCGTGAATCTCCCTCCGAGCGCCCGGTGATGACAGAGAAC 420
DB 361 AAGGTGAAGTTCAATCGGCGTGAATCTCCCTCCGAGCGCCCGGTGATGACAGAGAAC 420
QY 421 ATGGCTGGGAGGCTTCCACGAGCGCTGTACCCCGCGAGCGGTGTCTGAAGGGCGAG 480
DB 421 ATGGCTGGGAGGCTTCCACGAGCGCTGTACCCCGCGAGCGGTGTCTGAAGGGCGAG 480
QY 481 ATCCACAAGGCTCTGAAGCTGAAGGACGCGCGGACCTACCTGTTGAGTTCAAGTCCATC 540
DB 481 ATCCACAAGGCTCTGAAGCTGAAGGACGCGCGGACCTACCTGTTGAGTTCAAGTCCATC 540
QY 541 TACATGGCCAAAGAACCCGTGCAAGCTGCGCGCTTACTACTGTTGAGTCAAGCTGAGC 600
DB 541 TACATGGCCAAAGAACCCGTGCAAGCTGCGCGCTTACTACTGTTGAGTCAAGCTGAGC 600
QY 601 ATCACTCTCCCAACAAGGACTGACCACTGCTGAGGACGTTGAGTCAAGCTGAGC 660
DB 601 ATCACTCTCCCAACAAGGACTGACCACTGCTGAGGACGTTGAGTCAAGCTGAGC 660
QY 661 CACCACTGTTCTCTGTAA 678
DB 661 CACCACTGTTCTCTGTAA 678
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RESULT 3

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US-10-315-920-5
; Sequence 5, Application US/10315920
; Publication No. US20030175809A1
; GENERAL INFORMATION:
; APPLICANT: Teresikh, Alexey
; APPLICANT: Fedorovich
; TITLE OF INVENTION: FLUORESCENT TIMER PROTEINS AND METHODS
; FILE REFERENCE: CLON-077CIP
```

CURRENT APPLICATION NUMBER: US/10/315,920
CURRENT FILING DATE: 2002-12-09
PRIOR APPLICATION NUMBER: 60/211,607
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: PCT/US01/19097
PRIOR FILING DATE: 2001-06-13
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 678
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: variant of sequence from Discosoma sp.
US-10-315-920-5

Query Match 99.8%; Score 676.4; DB 16; Length 678;
Best Local Similarity 99.9%; Pred. No. 5,4e-167;
Matches 677; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGCTCTCTCCGAGAAAGTATCAACGAGTTCAATGCGTTCAAGGTGCGCATGAGAGGC 60
DB 1 ATGGCTCTCTCCGAGAAAGTATCAACGAGTTCAATGCGTTCAAGGTGCGCATGAGAGGC 60
QY 61 ACCGTGAACGGGCGACAGATTGAGATCGAGGGCGAGGGCGAGGGCGGCCCTTACGAGGGGC 120
DB 61 ACCGTGAACGGGCGACAGATTGAGATCGAGGGCGAGGGCGAGGGCGGCCCTTACGAGGGGC 120
QY 121 CACAACACCGTGAAGTTGAAGGTGACCAAGGGCGGCGCCCTGCGCTTGCGCTGGAGATC 180
DB 121 CACAACACCGTGAAGTTGAAGGTGACCAAGGGCGGCGCCCTGCGCTTGCGCTGGAGATC 180
QY 121 CACAACACCGTGAAGTTGAAGGTGACCAAGGGCGGCGCCCTGCGCTTGCGCTGGAGATC 180
DB 121 CACAACACCGTGAAGTTGAAGGTGACCAAGGGCGGCGCCCTGCGCTTGCGCTGGAGATC 180
QY 181 CTGTCTCCCGGAGTTCAAGTACGGCTCTCAAGGTGACGTTGAGAGACCCCGCGCATCTCC 240
DB 181 CTGTCTCCCGGAGTTCAAGTACGGCTCTCAAGGTGACGTTGAGAGACCCCGCGCATCTCC 240
QY 241 GACTACAGAAGAGTCTCTCCCGAGGGGCTTCAAGTGGAGCGGCTGATGAACTTCGAG 300
DB 241 GACTACAGAAGAGTCTCTCCCGAGGGGCTTCAAGTGGAGCGGCTGATGAACTTCGAG 300
QY 301 GACGCGCGCGTGGCGACCGGTGACCCAGGACTCTCTCTGCAAGACCGGCTGCTTCACTTAC 360
DB 301 GACGCGCGCGTGGCGACCGGTGACCCAGGACTCTCTCTGCAAGACCGGCTGCTTCACTTAC 360
QY 301 GACGCGCGCGTGGCGACCGGTGACCCAGGACTCTCTCTGCAAGACCGGCTGCTTCACTTAC 360
DB 301 GACGCGCGCGTGGCGACCGGTGACCCAGGACTCTCTCTGCAAGACCGGCTGCTTCACTTAC 360
QY 361 AAGGTGAAGTTCAATCGGCGGTGAACTTCCCTTCCAGCGGCGCCGCTGATGAGAAAGACC 420
DB 361 AAGGTGAAGTTCAATCGGCGGTGAACTTCCCTTCCAGCGGCGCCGCTGATGAGAAAGACC 420
QY 421 ATGGGCTGGAGAGGCTCTCCACGAGCGGCTGTACCCCGCGAGCGGCTGTGAAGGGCGAG 480
DB 421 ATGGGCTGGAGAGGCTCTCCACGAGCGGCTGTACCCCGCGAGCGGCTGTGAAGGGCGAG 480
QY 481 ATCCACAAAGGCGCTGAGAGCTGAAAGACGCGCGGCACTACTGTGTGAGAGTTCAAGTCCATC 540
DB 481 ATCCACAAAGGCGCTGAGAGCTGAAAGACGCGCGGCACTACTGTGTGAGAGTTCAAGTCCATC 540
QY 541 TACATGCGCAAGAAAGCCCGTGAAGTCTGCGCGCTTCTACTACTGTGAGACCAAGCTGAGAC 600
DB 541 TACATGCGCAAGAAAGCCCGTGAAGTCTGCGCGCTTCTACTACTGTGAGACCAAGCTGAGAC 600
QY 601 ATCACTCTCCCAACAGAGACTACACCATCTGTGAGAGAGTACGAGCGACCGAGGGGCGGC 660
DB 601 ATCACTCTCCCAACAGAGACTACACCATCTGTGAGAGAGTACGAGCGACCGAGGGGCGGC 660
QY 661 CACCACTGTCTCTGTAA 678
DB 661 CACCACTGTCTCTGTAA 678

RESULT 4
US-10-060-857-7
Sequence 7, Application US/10060857
Publication No. US20020132318A1

GENERAL INFORMATION:
APPLICANT: Anticancer, Inc.
APPLICANT: Zhao, Ming
APPLICANT: Jiang, Ping
APPLICANT: Xu, Mingxu
APPLICANT: Yang, Meng
TITLE OF INVENTION: IMPROVED FLUORESCENT PROTEINS
FILE REFERENCE: 31276-20032.00
CURRENT APPLICATION NUMBER: US/10/060,857
CURRENT FILING DATE: 2002-01-29
PRIOR APPLICATION NUMBER: US 60/264,932
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 1050
TYPE: DNA
ORGANISM: Coral
US-10-060-857-7

Query Match 99.1%; Score 672.2; DB 13; Length 1050;
Best Local Similarity 99.6%; Pred. No. 6,9e-166;
Matches 674; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGGCTCTCTCCGAGAAAGTATCAACGAGTTCAATGCGTTCAAGGTGCGCATGAGAGGC 60
DB 289 ATGGCTCTCTCCGAGAAAGTATCAACGAGTTCAATGCGTTCAAGGTGCGCATGAGAGGC 348
QY 61 ACCGTGAACGGGCGACAGATTGAGATCGAGGGCGAGGGCGAGGGCGGCCCTTACGAGGGGC 120
DB 349 ACCGTGAACGGGCGACAGATTGAGATCGAGGGCGAGGGCGAGGGCGGCCCTTACGAGGGGC 408
QY 121 CACAACACCGTGAAGTTGAAGGTGACCAAGGGCGGCGCCCTGCGCTTGCGCTGGAGATC 180
DB 349 CACAACACCGTGAAGTTGAAGGTGACCAAGGGCGGCGCCCTGCGCTTGCGCTGGAGATC 408
QY 121 CACAACACCGTGAAGTTGAAGGTGACCAAGGGCGGCGCCCTGCGCTTGCGCTGGAGATC 180
DB 409 CACAACACCGTGAAGTTGAAGGTGACCAAGGGCGGCGCCCTGCGCTTGCGCTGGAGATC 468
QY 181 CTGTCTCCCGGAGTTCAAGTACGGCTCTCAAGGTGACGTTGAGAGACCCCGCGCATCTCC 240
DB 469 CTGTCTCCCGGAGTTCAAGTACGGCTCTCAAGGTGACGTTGAGAGACCCCGCGCATCTCC 528
QY 241 GACTACAGAAGAGTCTCTCCCGAGGGGCTTCAAGTGGAGCGGCTGATGAACTTCGAG 300
DB 529 GACTACAGAAGAGTCTCTCCCGAGGGGCTTCAAGTGGAGCGGCTGATGAACTTCGAG 588
QY 301 GACGCGCGCGTGGCGACCGGTGACCCAGGACTCTCTCTGCAAGACCGGCTGCTTCACTTAC 360
DB 589 GACGCGCGCGTGGCGACCGGTGACCCAGGACTCTCTCTGCAAGACCGGCTGCTTCACTTAC 648
QY 361 AAGGTGAAGTTCAATCGGCGGTGAACTTCCCTTCCAGCGGCGCCGCTGATGAGAAAGACC 420
DB 649 AAGGTGAAGTTCAATCGGCGGTGAACTTCCCTTCCAGCGGCGCCGCTGATGAGAAAGACC 708
QY 421 ATGGGCTGGAGAGGCTCTCCACGAGCGGCTGTACCCCGCGAGCGGCTGTGAAGGGCGAG 480
DB 709 ATGGGCTGGAGAGGCTCTCCACGAGCGGCTGTACCCCGCGAGCGGCTGTGAAGGGCGAG 768
QY 481 ATCCACAAAGGCGCTGAGAGCTGAAAGACGCGCGGCACTACTGTGTGAGAGTTCAAGTCCATC 540
DB 769 ATCCACAAAGGCGCTGAGAGCTGAAAGACGCGCGGCACTACTGTGTGAGAGTTCAAGTCCATC 828
QY 541 TACATGCGCAAGAAAGCCCGTGAAGTCTGCGCGCTTCTACTACTGTGAGACCAAGCTGAGAC 600
DB 829 TACATGCGCAAGAAAGCCCGTGAAGTCTGCGCGCTTCTACTACTGTGAGACCAAGCTGAGAC 888
QY 601 ATCACTCTCCCAACAGAGACTACACCATCTGTGAGAGAGTACGAGCGACCGAGGGGCGGC 660
DB 889 ATCACTCTCCCAACAGAGACTACACCATCTGTGAGAGAGTACGAGCGACCGAGGGGCGGC 948
QY 661 CACCACTGTCTCTGTAA 677
DB 949 CACCACTGTCTCTGTAA 965

Db 421 ATGGCTGGGAGGACCTCCACCGAGCGCTGTACCCCGGACGCGCTGTGAAGGGCGAG 480
Qy 481 ATCCCAAGAGCCCTTGAAGCTGAAGAGACGGCGGCACTACTTGTGTGAAGTTCAAGTCCATC 540
Db 481 ACCCAAGAGCCCTTGAAGCTGAAGAGACGGCGGCACTACTTGTGTGAAGTTCAAGTCCATC 540
Qy 541 TACATGGCCAGAGAGCCGCTGAGCTGCGGCGTACTACTACTGTGAACACCAAGCTGAC 600
Db 541 TACATGGCCAGAGAGCCGCTGAGCTGCGGCGTACTACTACTGTGAACACCAAGCTGAC 600
Qy 601 ATCACTCCCAACAGAGACTACACCATGTGAGACAGTACAGGCGACCGAGGGCGCG 660
Db 601 ATCACTCCCAACAGAGACTACACCATGTGAGACAGTACAGGCGACCGAGGGCGCG 660
Qy 661 CACCACTGTCTCTG 675
Db 661 CACCACTGTCTCTG 675

RESULT 7

US-10-081-864-13
; Sequence 13, Application US/10081864
; Publication No. US20030022287A1
; GENERAL INFORMATION:
; APPLICANT: Lukyanov, Sergey
; APPLICANT: Yushmanov, Konstantin
; APPLICANT: Yushmanov, Yuriy
; APPLICANT: Savitsky, Alexander
; APPLICANT: Pradkov, Arcady
; TITLE OF INVENTION: No. US20030022287A1 Aggregating Fluorescent Proteins and
; FILE REFERENCE: C10N-067
; CURRENT APPLICATION NUMBER: US/10/081,864
; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: 10/006,922
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/270,983
; PRIOR FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 675
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: non-aggregating mutant
US-10-081-864-13

Query Match 98.8%; Score 670.2; DB 14; Length 675;
Best Local Similarity 99.6%; Pred. No. 2.2e-165;
Matches 672; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 ATGGCTCTCTCCGAGAGCTCATCACCGAGTTCAAGCTGCGCATGAGGGC 60
Db 1 ATGGCTCTCTCCGAGAGAGCTCATCACCGAGTTCAAGCTGCGCATGAGGGC 60
Qy 61 ACCGTGAACGGCCAGAGTTGAGATCGAGGCGAGGGCGGCGGCTTACGAGGGC 120
Db 61 ACCGTGAACGGCCAGAGTTGAGATCGAGGCGAGGGCGGCGGCTTACGAGGGC 120
Qy 121 CACAACACCGTGAAGTTGAAGGTGACCAAGGGCGGCGGCTTCCGCTGAGGACATC 180
Db 121 CACAACACCGTGAAGTTGAAGGTGACCAAGGGCGGCGGCTTCCGCTGAGGACATC 180
Qy 181 CTGTCCCTCCAGTTCCAGTACGGCTCAAGGTGTAGTGAAGCAACCGCGCATCCCC 240
Db 181 CTGTCCCTCCAGTTCCAGTACGGCTCAAGGTGTAGTGAAGCAACCGCGCATCCCC 240
Qy 241 GACTACAAAGAGTGTCTTCCCGAGGGCTTCAATGGGAGGGCTGTGAATCTTCAG 300
Db 241 GACTACAAAGAGTGTCTTCCCGAGGGCTTCAATGGGAGGGCTGTGAATCTTCAG 300
Qy 301 GACGGGGGGGTGGAGACCGTGAACCGAGACTCTCTCTGAGAGGACGGCTGTATCTAC 360

Db 301 GACGGGGGGGTGGAGACCGTGAACCGAGACTCTCTCTGAGAGGAGGGCTGTATCTAC 360
Qy 361 AAGGTGAAGTTCAATGGGCGTGAAGTTCCCTCCGACGCGCCGTGTATGCAAGAGACC 420
Db 361 AAGGTGAAGTTCAATGGGCGTGAAGTTCCCTCCGACGCGCCGTGTATGCAAGAGACC 420
Qy 421 ATGGCTGGGAGGACCTCCACCGAGGCGCTGTATCCCGGACGAGGGGTGTGAAGGGCGAG 480
Db 421 ATGGCTGGGAGGACCTCCACCGAGGCGCTGTATCCCGGACGAGGGGTGTGAAGGGCGAG 480
Qy 481 ATCCCAAGAGCCCTTGAAGCTGAAGAGACGGCGGCACTACTTGTGTGAAGTTCAAGTCCATC 540
Db 481 ACCCAAGAGCCCTTGAAGCTGAAGAGACGGCGGCACTACTTGTGTGAAGTTCAAGTCCATC 540
Qy 541 TACATGGCCAGAGAGCCGCTGAGCTGCGGCGTACTACTACTGTGAACACCAAGCTGAC 600
Db 541 TACATGGCCAGAGAGCCGCTGAGCTGCGGCGTACTACTACTGTGAACACCAAGCTGAC 600
Qy 601 ATCACTCCCAACAGAGACTACACCATGTGAGACAGTACAGGCGACCGAGGGCGCG 660
Db 601 ATCACTCCCAACAGAGACTACACCATGTGAGACAGTACAGGCGACCGAGGGCGCG 660
Qy 661 CACCACTGTCTCTG 675
Db 661 CACCACTGTCTCTG 675

RESULT 8

US-10-785-862-10
; Sequence 10, Application US/10785862
; Publication No. US20040261149A1
; GENERAL INFORMATION:
; APPLICANT: Donald Danforth Plant Science Center
; APPLICANT: Fauguet, Claude M.
; APPLICANT: Padmanabhan, Chellappan
; APPLICANT: Ramachandran, Vaniharani
; TITLE OF INVENTION: siRNA-mediated inhibition of gene expression in plant cells
; FILE REFERENCE: C35621/104850
; CURRENT APPLICATION NUMBER: US/10/785,862
; CURRENT FILING DATE: 2004-02-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 747
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: the deRed coding sequence
US-10-785-862-10

Query Match 98.8%; Score 670.2; DB 18; Length 747;
Best Local Similarity 99.6%; Pred. No. 2.2e-165;
Matches 672; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 ATGGCTCTCTCCGAGAGCTCATCACCGAGTTCAAGCTGCGCATGAGGGC 60
Db 1 ATGGCTCTCTCCGAGAGCTCATCACCGAGTTCAAGCTGCGCATGAGGGC 60
Qy 61 ACCGTGAACGGCCAGAGTTGAGATCGAGGCGAGGGCGGCGGCTTACGAGGGC 120
Db 61 ACCGTGAACGGCCAGAGTTGAGATCGAGGCGAGGGCGGCGGCTTACGAGGGC 120
Qy 121 CACAACACCGTGAAGTTGAAGGTGACCAAGGGCGGCGGCTTCCGCTGAGGACATC 180
Db 121 CACAACACCGTGAAGTTGAAGGTGACCAAGGGCGGCGGCTTCCGCTGAGGACATC 180
Qy 181 CTGTCCCTCCAGTTCCAGTACGGCTCAAGGTGTAGTGAAGCAACCGCGCATCCCC 240
Db 181 CTGTCCCTCCAGTTCCAGTACGGCTCAAGGTGTAGTGAAGCAACCGCGCATCCCC 240
Qy 241 GACTACAAAGAGTGTCTTCCCGAGGGCTTCAATGGGAGGGCTGTGAATCTTCAG 300

Db 241 GACTACAGAAGCTGTCTTCCCGAGGGCTTCAAGTGGAGCGCGTGAATGAATTTCGAG 300
Qy 301 GACGGCGCGGTGGAGACCGGTACAGGACCTCTCCGAGAGACGGCTGCTTCACTAC 360
Db 301 GACGGCGCGGTGGAGACCGGTACAGGACCTCTCCGAGAGACGGCTGCTTCACTAC 360
Qy 361 AAGGTGAAGTTCATCGGCGTGAATCTCCCTCCGAGCGCCCGGTGATGACAGAGAAC 420
Db 361 AAGGTGAAGTTCATCGGCGTGAATCTCCCTCCGAGCGCCCGGTGATGACAGAGAAC 420
Qy 421 ATGGGCTGGAGGCTTCCACGAGCGCTGTACCCCGGACGGCGTGTCTGAAGGGCGAG 480
Db 421 ATGGGCTGGAGGCTTCCACGAGCGCTGTACCCCGGACGGCGTGTCTGAAGGGCGAG 480
Qy 481 ATCCACAAGGCGCTGAAGCTGAAGGAGCGGCGCACTACCTGTGAGTTCAGTTCATC 540
Db 481 ATCCACAAGGCGCTGAAGCTGAAGGAGCGGCGCACTACCTGTGAGTTCAGTTCATC 540
Qy 541 TACATGGCCAAAGACCCGTCAGCTGCGGCTACTACTAGTGAACCAAGCTGAGC 600
Db 541 TACATGGCCAAAGACCCGTCAGCTGCGGCTACTACTAGTGAACCAAGCTGAGC 600
Qy 601 ATCACTTCCCAACAAGAGACTACCACTGTGAGACGTACAGCGCACGAGGGCGGC 660
Db 601 ATCACTTCCCAACAAGAGACTACCACTGTGAGACGTACAGCGCACGAGGGCGGC 660
Qy 661 CACCACTGTTCCTG 675
Db 661 CACCACTGTTCCTG 675

RESULT 9

US-10-315-920-3
; Sequence 3, Application US/10315920
; Publication No. US20030175809A1
; GENERAL INFORMATION:
; APPLICANT: Fradkov, Arcady Fedorovich
; APPLICANT: Tersikh, Alexey
; TITLE OF INVENTION: FLUORESCENT TIMER PROTEINS AND METHODS
; TITLE OF INVENTION: FOR THEIR USE
; FILE REFERENCE: CLON-077CIP
; CURRENT APPLICATION NUMBER: US/10/315,920
; PRIOR FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: 60/211,607
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: PCT/US01/19097
; PRIOR FILING DATE: 2001-06-13
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 678
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: variant of sequence from Discosoma sp.
; US-10-315-920-3

Query Match 98.6%; Score 668.4; DB 16; Length 678;
Best Local Similarity 99.1%; Pred. No. 6.6e-165;
Matches 672; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ATGGCTCTCTCCGAAAGTTCATCAAGATTTCAGTTCAGAGTGGCGATGAGAGGC 60
Db 1 ATGGCTCTCTCCGAAAGTTCATCAAGATTTCAGTTCAGAGTGGCGATGAGAGGC 60
Qy 61 ACCGTGAACGGCCACGAGTTGAGATGAGGGCGAGGGCGCGCCCTTACGAGGGC 120
Db 61 ACCGTGAACGGCCACGAGTTGAGATGAGGGCGAGGGCGCGCCCTTACGAGGGC 120
Qy 121 CACAACACCGTGAAGTGAAGGTGACCAAGGGCGGGCCCGCTTGCCTGAGACATC 180
Db 121 CACAACACCGTGAAGTGAAGGTGACCAAGGGCGGGCCCGCTTGCCTGAGACATC 180

Qy 181 CTGTCCCCAGTTCAGTACGGCTCCAGAGGTGATGAGACACCCCGGACATCC 240
Db 181 CTGTCCCCAGTTCAGTACGGCTCCAGAGGTGATGAGACACCCCGGACATCC 240
Qy 241 GACTACAAAGACTGTCTTCCCGAGGGCTTCAAGTGGAGCGCGTGAATGAATTTCGAG 300
Db 241 GACTACAAAGACTGTCTTCCCGAGGGCTTCAAGTGGAGCGCGTGAATGAATTTCGAG 300
Qy 301 GACGGCGCGGTGGAGACCGGTACAGGACCTCTCCGAGAGCGCCCGGTGATGAACTTCGAG 360
Db 301 GACGGCGCGGTGGAGACCGGTACAGGACCTCTCCGAGAGCGCCCGGTGATGAACTTCGAG 360
Qy 361 AAGGTGAAGTTCATCGGCGTGAATCTCCCTCCGAGCGCCCGGTGATGACAGAGAAC 420
Db 361 AAGGTGAAGTTCATCGGCGTGAATCTCCCTCCGAGCGCCCGGTGATGACAGAGAAC 420
Qy 421 ATGGGCTGGAGGCTTCCACGAGCGCTGTACCCCGGACGGCGTGTCTGAAGGGCGAG 480
Db 421 ATGGGCTGGAGGCTTCCACGAGCGCTGTACCCCGGACGGCGTGTCTGAAGGGCGAG 480
Qy 481 ATCCACAAGGCGCTGAAGCTGAAGGAGCGGCGCACTACCTGTGAGTTCAGTTCATC 540
Db 481 ATCCACAAGGCGCTGAAGCTGAAGGAGCGGCGCACTACCTGTGAGTTCAGTTCATC 540
Qy 541 TACATGGCCAAAGACCCGTCAGCTGCGGCTACTACTAGTGAACCAAGCTGAGC 600
Db 541 TACATGGCCAAAGACCCGTCAGCTGCGGCTACTACTAGTGAACCAAGCTGAGC 600
Qy 601 ATCACTTCCCAACAAGAGACTACCACTGTGAGACGTACAGCGCACGAGGGCGGC 660
Db 601 ATCACTTCCCAACAAGAGACTACCACTGTGAGACGTACAGCGCACGAGGGCGGC 660
Qy 661 CACCACTGTTCCTGTA 678
Db 661 CACCACTGTTCCTGTA 678

RESULT 10

US-10-742-828-4
; Sequence 4, Application US/10742828
; Publication No. US20040157294A1
; GENERAL INFORMATION:
; APPLICANT: Heintich, Gerhard
; APPLICANT: Hynh, Gigi
; TITLE OF INVENTION: TRANSGENIC SCREEN AND METHOD FOR SCREENING MODULATORS OF BRAIN-DE
; TITLE OF INVENTION: 1353/03 (VA)
; FILE REFERENCE: US 10/306,737
; CURRENT APPLICATION NUMBER: US/10/742,828
; PRIOR FILING DATE: 2003-12-23
; PRIOR APPLICATION NUMBER: US 10/306,737
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 4
; LENGTH: 7508
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Unsure
; LOCATION:
; OTHER INFORMATION: Synthesized
; US-10-742-828-4

Query Match 98.3%; Score 666.4; DB 18; Length 7508;
Best Local Similarity 99.1%; Pred. No. 2.5e-164;
Matches 670; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 TGGCTCTCTCCGAAAGTTCATCAAGATTTCAGTTCAGAGTGGCGATGAGAGGC 61
Db 2124 TGGCTCTCTCCGAAAGTTCATCAAGATTTCAGTTCAGAGTGGCGATGAGAGGC 2183
Qy 62 CCGTGAACGGCCACGAGTTGAGATGAGGGCGAGGGCGCGCCCTTACGAGGGC 121
Db 2184 CCGTGAACGGCCACGAGTTGAGATGAGGGCGAGGGCGCGCCCTTACGAGGGC 2243

122 ACAACACGGTGAAGTTGAAGTGAACCAAGGGGCGCCCTGCTTCCCTGGAGCATCC 181
DB ACAACACGGTGAAGTTGAAGTGAACCAAGGGGCGCCCTGCTTCCCTGGAGCATCC 2303
QY 182 TGTCCCTGAGTTCCAGTACGAGCTCCCAAGTGTGAGAGCACTCCGCGCATCCCG 241
DB 2304 TGTCCCTGAGTTCCAGTACGAGCTCCCAAGTGTGAGAGCACTCCGCGCATCCCG 2363
QY 242 ACTACAAAGAGTGTCTTCCCTCCGAGGGCTTCAAGTGGAGAGCGGTGATGAAGCTTCGAG 301
DB 2364 ACTACAAAGAGTGTCTTCCCTCCGAGGGCTTCAAGTGGAGAGCGGTGATGAAGCTTCGAG 2423
QY 302 ACGGCGGCGTGGCGACCGGTGACCAAGTCTCTCCCTGAGAGAGCGCTTCACTTACA 361
DB 2424 ACGGCGGCGTGGCGACCGGTGACCAAGTCTCTCCCTGAGAGAGCGCTTCACTTACA 2483
QY 362 AAGTGAAGTTCAATCGGCGGTGAATCTTCCCTCCGAGCGCCCGGTGATGCAAGAGAACCA 421
DB 2484 AAGTGAAGTTCAATCGGCGGTGAATCTTCCCTCCGAGCGCCCGGTGATGCAAGAGAACCA 2543
QY 422 TGGGCTGGAGAGGCTTCCACCGAGCGCTGTATACCCCGCGAGCGGCTGTGAAGGGCGAGA 481
DB 2544 TGGGCTGGAGAGGCTTCCACCGAGCGCTGTATACCCCGCGAGCGGCTGTGAAGGGCGAGA 2603
QY 482 TCCACAAGGCGCTGAAGTGAAGAGAGCGGCGCACTACCTGTGAGAGTTCAAGTCAATCT 541
DB 2604 TCCACAAGGCGCTGAAGTGAAGAGAGCGGCGCACTACCTGTGAGAGTTCAAGTCAATCT 2663
QY 542 ACATGAGCCAAAGAGCGCGTGCAGCTGCCGCGTACTACTACGTGAGCAACCAAGCTGAGCA 601
DB 2664 ACATGAGCCAAAGAGCGCGTGCAGCTGCCGCGTACTACTACGTGAGCAACCAAGCTGAGCA 2723
QY 602 TCACTCTCCCAACAGAGCTACACCATGTGTGAGAGAGAGCGCAACCGAGGGCGGCG 661
DB 2724 TCACTCTCCCAACAGAGCTACACCATGTGTGAGAGAGAGCGCAACCGAGGGCGGCG 2783
QY 662 ACCACCTGTCTCTGTA 677
DB 2784 ACCACCTGTCTCTGTA 2799

RESULT 11

US-10-081-864-7
; Sequence 7, Application US/10081864
; Publication No. US2003002287A1
; GENERAL INFORMATION:
; APPLICANT: Lukanov, Sergey
; APPLICANT: Lukanov, Konstantin
; APPLICANT: Yarushevich, Yuriy
; APPLICANT: Savitsky, Alexander
; APPLICANT: Fradkov, Arcady
; TITLE OF INVENTION: No. US2003002287A1 Aggregating Fluorescent Proteins and
; FILE REFERENCE: CLON-067
; CURRENT APPLICATION NUMBER: US/10/081,864
; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: 10/006,922
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/270,983
; PRIOR FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FaSTSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 678
; TYPE: DNA
; ORGANISM: *Dicobosoma* sp
US-10-081-864-7

Query Match 98.1%; Score 665.2; DB 14; Length 678;
Best Local Similarity 98.8%; Pred. No. 4.5e-164;
Matches 670; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 1 ATGGCTCTCTCGAAGAGCTCATCAGGTTTCATGCGCTTCAAGGTGCGCATGAGAGGCG 60

1 ATGGCTCTCTCGAAGAGCTCATCAGGTTTCATGCGCTTCAAGGTGCGCATGAGAGGCG 60
DB 61 ACCGTGAACGGCCACAGATTTGAGATCGAGGGCGAGGGCGAGGGCGCCCTTACAGAGGGC 120
QY 61 ACCGTGAACGGCCACAGATTTGAGATCGAGGGCGAGGGCGAGGGCGCCCTTACAGAGGGC 120
DB 121 CACAAACCGTGAAGTTGAAGTGAACCAAGGGGCGCCCTGCTTCCCTGCTTGGAGATC 180
QY 121 CACAAACCGTGAAGTTGAAGTGAACCAAGGGGCGCCCTGCTTCCCTGCTTGGAGATC 180
DB 181 CTGTCCCTCCAGTTCCAGTACCGCTCCAGGTTGTAAGTGAAGCACTCCGCGCATATCCC 240
QY 181 CTGTCCCTCCAGTTCCAGTACCGCTCCAGGTTGTAAGTGAAGCACTCCGCGCATATCCC 240
DB 241 GACTTCAAGAGAGCTGTCTTCCCGAGGGCTTCAAGTGGAGAGCGGTGATGAAGCTTCGAG 300
QY 241 GACTTCAAGAGAGCTGTCTTCCCGAGGGCTTCAAGTGGAGAGCGGTGATGAAGCTTCGAG 300
DB 301 GACGCGGCGGTGGAGCGGTGACCCAGGACTCTCTCCGAGAGAGCGGCTTCACTTAC 360
QY 301 GACGCGGCGGTGGAGCGGTGACCCAGGACTCTCTCCGAGAGAGCGGCTTCACTTAC 360
DB 361 AAGTGAAGTTCAATCGGCGGTGAATCTTCCCTCCGAGCGCCCGGTGATGCAAGAGAAC 420
QY 361 AAGTGAAGTTCAATCGGCGGTGAATCTTCCCTCCGAGCGCCCGGTGATGCAAGAGAAC 420
DB 421 ATGGCTGGAGAGGCTTCCACCGAGCGCTGTATACCCCGCGAGAGGCTGTGAGAGGGCGAG 480
QY 421 ATGGCTGGAGAGGCTTCCACCGAGCGCTGTATACCCCGCGAGAGGCTGTGAGAGGGCGAG 480
DB 421 ATGGCTGGAGAGGCTTCCACCGAGCGCTGTATACCCCGCGAGAGGCTGTGAGAGGGCGAG 480
QY 481 ATCCAAAGGCGCTGAAGTGAAGAGAGCGGCGCACTACCTGTGAGAGTTCAAGTCAATC 540
DB 481 ATCCAAAGGCGCTGAAGTGAAGAGAGCGGCGCACTACCTGTGAGAGTTCAAGTCAATC 540
QY 541 TACATGAGCCAAAGAGCGCGTGCAGCTGCCGCGTACTACTACGTGAGCAACCAAGCTGAG 600
DB 541 TACATGAGCCAAAGAGCGCGTGCAGCTGCCGCGTACTACTACGTGAGCAACCAAGCTGAG 600
QY 601 ATACCTCTCCCAACAGAGCTACACCATGTGTGAGAGAGAGCGCAACCGAGGGCGGCG 660
DB 601 ATACCTCTCCCAACAGAGCTACACCATGTGTGAGAGAGAGCGCAACCGAGGGCGGCG 660
QY 661 CACCACTGTCTCTGTA 678
DB 661 CACCACTGTCTCTGTA 678

RESULT 12

US-10-315-920-1
; Sequence 1, Application US/10315920
; Publication No. US20030175809A1
; GENERAL INFORMATION:
; APPLICANT: Fradkov, Arcady Fedorovich
; APPLICANT: Terelikh, Alexey
; TITLE OF INVENTION: FLUORESCENT TIMER PROTEINS AND METHODS
; FILE REFERENCE: CLON-077CIP
; CURRENT APPLICATION NUMBER: US/10/315,920
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: 60/211,607
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: PCT/US01/19097
; PRIOR FILING DATE: 2001-06-13
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FaSTSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 678
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: variant of sequence from *Dicobosoma* sp.
US-10-315-920-1

Query Match 98.1%; Score 665.2; DB 16; Length 678;
Best Local Similarity 98.8%; Pred. No. 4.5e-164;
Matches 670; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

```
QY 1 ATGCTCTCTCCGAGAACGTATCAACCGATTGATGCGCTTCAAGTGCAGATGAGAGGC 60
DB 1 ATGCGCTCTCTCCAGAGAACGTATCAAGAGATTGATGCGCTTCAAGTGCAGATGAGAGGC 60
QY 61 ACCGGAACCGGCGACGATTCGAGATTCGAGGGCGAGGGCGGCGCCCTTACAGAGGC 120
DB 61 ACCGGAACCGGCGACGATTCGAGATTCGAGGGCGAGGGCGGCGCCCTTACAGAGGC 120
QY 121 CACAACACCGTGAAGTTGAAGTGAACCAAGGGCGGCGCCCTTGCCTTGGCTGGAGATC 180
DB 121 CACAACACCGTGAAGTTGAAGTGAACCAAGGGCGGCGCCCTTGCCTTGGCTGGAGATC 180
QY 181 CTGTCCCGCCGATTCGATGAGGCTCAAGGTTGACGTTGAGACACCCCGGACATCCCC 240
DB 181 CTGTCCCGCCGATTCGATGAGGCTCAAGGTTGACGTTGAGACACCCCGGACATCCCC 240
QY 241 GACTACAAAGAGCTGTCTTCCCGAGGGCTTCAAGTGGAGCGGTGATGAATTCGAG 300
DB 241 GACTACAAAGAGCTGTCTTCCCGAGGGCTTCAAGTGGAGCGGTGATGAATTCGAG 300
QY 301 GACGCGCGCGTGGCGACCGTGAACCGAGACTCTTCCCTGACAGACGCGCTTCACTAC 360
DB 301 GACGCGCGCGTGGCGACCGTGAACCGAGACTCTTCCCTGACAGACGCGCTTCACTAC 360
QY 361 AAGGTGAAGTTGATGCGGCTGAATCTTCCCTCCGAGCGCCCGGTGATCAAGAGAACCC 420
DB 361 AAGGTGAAGTTGATGCGGCTGAATCTTCCCTCCGAGCGCCCGGTGATCAAGAGAACCC 420
QY 421 ATGGCTGGGAGGCTTCCACGAGCGCTGTACCCCGCGACGCGCTGTAAAGGGCGAG 480
DB 421 ATGGCTGGGAGGCTTCCACGAGCGCTGTACCCCGCGACGCGCTGTAAAGGGCGAG 480
QY 481 ATCCACAAGGCGCTGAAAGCTGAAGAGACGCGCGCCACTACTGTGAGATTCAAGTCATC 540
DB 481 ATCCACAAGGCGCTGAAAGCTGAAGAGACGCGCGCCACTACTGTGAGATTCAAGTCATC 540
QY 541 TACATGGCCAAAGAACCCGTGACGCTGCGGCTACTACTAGTGAACCTCAAGCTGAGAC 600
DB 541 TACATGGCCAAAGAACCCGTGACGCTGCGGCTACTACTAGTGAACCTCAAGCTGAGAC 600
QY 601 ATCACTCTCCCAAGAGAGACTACACATCGTGAAGAGTACGAGCGACCGAGGGCGGC 660
DB 601 ATCACTCTCCCAAGAGAGACTACACATCGTGAAGAGTACGAGCGACCGAGGGCGGC 660
QY 661 CACCACTGTTCCTGTAA 678
DB 661 CACCACTGTTCCTGTAA 678
```

RESULT 13
US-10-121-258-3

; Sequence 3, Application US/10121258
; Publication No. US20030059835A1
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger
; TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
; FILE REFERENCE: UC083.1CP2CPI
; CURRENT FILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: 09/794,308
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 09/866,538
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3

; LENGTH: 681
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: nucleotide sequence encoding DsRed with mammalian
US-10-121-258-3

Query Match 97.6%; Score 661.6; DB 14; Length 681;
Best Local Similarity 98.7%; Pred. No. 3.9e-163;
Matches 667; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

```
QY 2 TGGCTCTCTCCGAGAACGTATCAACCGATTGATGCGCTTCAAGTGCAGATGAGAGGC 61
DB 5 TGGCTCTCTCCGAGAACGTATCAAGAGATTGATGCGCTTCAAGTGCAGATGAGAGGC 64
QY 62 CCGTGAACGCGCAAGATTCGAGATTCGAGGGCGAGGGCGGCGCCCTTACAGAGGC 121
DB 62 CCGTGAACGCGCAAGATTCGAGATTCGAGGGCGAGGGCGGCGCCCTTACAGAGGC 124
QY 122 ACAACACCGTGAAGTTGAAGTGAACCAAGGGCGGCGCCCTTGCCTTGGAGATTC 181
DB 125 ACAACACCGTGAAGTTGAAGTGAACCAAGGGCGGCGCCCTTGCCTTGGAGATTC 184
QY 182 TGTCCCGCCGATTCAGTACGCGCTCAAGGTTGACGTTGAGACACCCCGGACATCCCG 241
DB 185 TGTCCCGCCGATTCAGTACGCGCTCAAGGTTGACGTTGAGACACCCCGGACATCCCG 244
QY 242 ACTTCAAGAGCTGTCTTCCCGAGGGCTTCAAGTGGAGCGGTGATGAATTCGAGG 301
DB 245 ACTTCAAGAGCTGTCTTCCCGAGGGCTTCAAGTGGAGCGGTGATGAATTCGAGG 304
QY 302 ACGGCGCGTGGCGACCGTGAACCGAGACTCTTCCCTGACAGACGCGCTTCACTACA 361
DB 305 ACGGCGCGTGGCGACCGTGAACCGAGACTCTTCCCTGACAGACGCGCTTCACTACA 364
QY 362 AAGTGAAGTTGATGCGGCTGAATCTTCCCTCCGAGCGCCCGGTGATCAAGAGAACCA 421
DB 365 AAGTGAAGTTGATGCGGCTGAATCTTCCCTCCGAGCGCCCGGTGATCAAGAGAACCA 424
QY 422 TGGGCTGGAGGCTTCCACGAGGCTGTACCCCGCGACGCGGTGCTGAAGGGCGAGA 481
DB 425 TGGGCTGGAGGCTTCCACGAGGCTGTACCCCGCGACGCGGTGCTGAAGGGCGAGA 484
QY 482 TCCACAAGGCGCTGAAGCTGAAGAGACGCGCGCCACTACTGTGAGATTCAAGTCATC 541
DB 485 TCCACAAGGCGCTGAAGCTGAAGAGACGCGCGCCACTACTGTGAGATTCAAGTCATC 544
QY 542 ACATGGCCAAAGAACCCGTGACGCTGCGGCTACTACTAGTGAACCAAGCTGAGACA 601
DB 545 ACATGGCCAAAGAACCCGTGACGCTGCGGCTACTACTAGTGAACCTCAAGCTGAGACA 604
QY 602 TCACCTCCCAACAGAGACTACACATCGTGAAGAGTACGAGCGACCGAGGGCGGCC 661
DB 605 TCACCTCCCAACAGAGACTACACATCGTGAAGAGTACGAGCGACCGAGGGCGGCC 664
QY 662 ACACCTGTTCCTGTAA 677
DB 665 ACACCTGTTCCTGTAA 680
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RESULT 14
US-10-121-258-23

; Sequence 23, Application US/10121258
; Publication No. US20030059835A1
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger
; TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
; FILE REFERENCE: UC083.1CP2CPI
; CURRENT FILING DATE: 2002-04-10

```

; PRIOR APPLICATION NUMBER: 09/794,308
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 09/866,538
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 681
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: nucleotide sequence encoding Dered with mammalian
; OTHER INFORMATION: codon usage
US-10-121-258-23

Query Match          97.6%; Score 661.6; DB 14; Length 681;
Best Local Similarity 98.7%; Pred. No. 3.9e-163;
Matches 667; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2 TGGCCCTCCCGAGAACGTCATCACCGAGTTGCGCTTCAAGGTGCGCATGAGAGCA 61
DB 5 TCGGCTCTCCCAAGAACGTCATCAAGAGATTCAATGCTTCAAGGTGCGCATGAGAGCA 64
QY 62 CCGTGAACGGCCACGAGATTGAGATCGAGGCGAGGCGAGGCGCCCTTACGAGGCGC 121
DB 65 CCGTGAACGGCCACGAGATTGAGATCGAGGCGAGGCGAGGCGCCCTTACGAGGCGC 124
QY 122 ACAACACCGTGAAAGTTGAAGTGACCAAGAGGCGGCGCCCTTGCCTTGCCTGAGACATCC 181
DB 125 ACAACACCGTGAAAGTTGAAGTGACCAAGAGGCGGCGCCCTTGCCTTGCCTGAGACATCC 184
QY 182 TGTCCCCCAGTTCCAGTACGGCTCCAGAGTGTACGTGAAGCAACCCCGCGACATCCCG 241
DB 185 TGTCCCCCAGTTCCAGTACGGCTCCAGAGTGTACGTGAAGCAACCCCGCGACATCCCG 244
QY 242 ACTACAGAGAGCTGTCTTCCCGCGAGGCTTCAAGTGAGGCGCGTGAATGAATTGAGG 301
DB 245 ACTACAGAGAGCTGTCTTCCCGCGAGGCTTCAAGTGAGGCGCGTGAATGAATTGAGG 304
QY 302 ACGGCGGCGTGCGAGACCGTGACCCAGAGACTCTCTCTGAGAGACGGCTGCTTCAATCTACA 361
DB 305 ACGGCGGCGTGCGAGACCGTGACCCAGAGACTCTCTCTGAGAGACGGCTGCTTCAATCTACA 364
QY 362 AGGTGAAGTTCAATCGGCGTGAATCTTCCCTCCGAGCGGCGCCCGTGAATGCAAGAAAGCA 421
DB 365 AGGTGAAGTTCAATCGGCGTGAATCTTCCCTCCGAGCGGCGCCCGTGAATGCAAGAAAGCA 424
QY 422 TGGGCTGGAGGCGCTTCAACCGAGCGCTGTACCCCGCGAGCGGCTGTAAGAGGCGAGA 481
DB 425 TGGGCTGGAGGCGCTTCAACCGAGCGCTGTACCCCGCGAGCGGCTGTAAGAGGCGAGA 484
QY 482 TTCACAGAGCGCTGAAGCTGAAGAGACGAGCGGCCACTACTGTGTGAGATTCAAGTCCATCT 541
DB 485 TTCACAGAGCGCTGAAGCTGAAGAGACGAGCGGCCACTACTGTGTGAGATTCAAGTCCATCT 544
QY 542 ACATGGCCCAAGAAAGCCCGTGCAGCTGCGCGGTACTTACTAGTGAACACCAAGCTGAGANA 601
DB 545 ACATGGCCCAAGAAAGCCCGTGCAGCTGCGCGGTACTTACTAGTGAACACCAAGCTGAGANA 604
QY 602 TCACCTCCCAACAGAGACTACACCATGTGAGAGAGTACGAGCGCACCGAGGCGCGCC 661
DB 605 TCACCTCCCAACAGAGACTACACCATGTGAGAGAGTACGAGCGCACCGAGGCGCGCC 664
QY 662 ACCACCTGTTCTCTGTA 677
DB 665 ACCACCTGTTCTCTGTA 680

RESULT 15
US-10-161-403-29
; Sequence 29, Application US/10161403
; Publication No. US20030119104A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Perkins, Edward
; APPLICANT: Perez, Carl
; APPLICANT: Lindendaum, Michael
; APPLICANT: Greene, Amy
; APPLICANT: Leung, Josephine
; APPLICANT: Fleming, Elena
; APPLICANT: Stewart, Sandra
; APPLICANT: Shellard, Joan
; TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
; FILE REFERENCE: 24601-420
; CURRENT APPLICATION NUMBER: US/10/161,403
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/294,758
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: 60/366,891
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 4692
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pdsred1-N1 plasmid from Clontech
US-10-161-403-29

Query Match          97.6%; Score 661.6; DB 15; Length 4692;
Best Local Similarity 98.7%; Pred. No. 4.4e-163;
Matches 667; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2 TGGCCCTCCCGAGAACGTCATCACCGAGTTGCGCTTCAAGGTGCGCATGAGAGCA 61
DB 683 TGGCTCTCTCCCAAGAACGTCATCAAGAGATTATGCTTCAAGGTGCGCATGAGAGCA 742
QY 62 CCGTGAACGGCCACGAGATTGAGATCGAGGCGAGGCGAGGCGCCCTTACGAGGCGC 121
DB 743 CCGTGAACGGCCACGAGATTGAGATCGAGGCGAGGCGAGGCGCCCTTACGAGGCGC 802
QY 122 ACAACACCGTGAAAGTTGAAGTGACCAAGAGGCGGCGCCCTTGCCTTGCCTGAGACATCC 181
DB 803 ACAACACCGTGAAAGTTGAAGTGACCAAGAGGCGGCGCCCTTGCCTTGCCTGAGACATCC 862
QY 182 TGTCCCCCAGTTCCAGTACGGCTCCAGAGTGTACGTGAAGCAACCCCGCGACATCCCG 241
DB 863 TGTCCCCCAGTTCCAGTACGGCTCCAGAGTGTACGTGAAGCAACCCCGCGACATCCCG 244
QY 242 ACTACAGAGAGCTGTCTTCCCGCGAGGCTTCAAGTGAGGCGCGTGAATGAATTGAGG 301
DB 923 ACTACAGAGAGCTGTCTTCCCGCGAGGCTTCAAGTGAGGCGCGTGAATGAATTGAGG 304
QY 302 ACGGCGGCGTGCGAGACCGTGACCCAGAGACTCTCTCTGAGAGACGGCTGCTTCAATCTACA 361
DB 983 ACGGCGGCGTGCGAGACCGTGACCCAGAGACTCTCTCTGAGAGACGGCTGCTTCAATCTACA 364
QY 362 AGGTGAAGTTCAATCGGCGTGAATCTTCCCTCCGAGCGGCGCGTGAATGCAAGAAAGCA 421
DB 1043 AGGTGAAGTTCAATCGGCGTGAATCTTCCCTCCGAGCGGCGCGTGAATGCAAGAAAGCA 424
QY 422 TGGGCTGGAGGCGCTTCAACCGAGCGCTGTACCCCGCGAGCGGCTGTAAGAGGCGAGA 481
DB 1103 TGGGCTGGAGGCGCTTCAACCGAGCGCTGTACCCCGCGAGCGGCTGTAAGAGGCGAGA 484
QY 482 TTCACAGAGCGCTGAAGCTGAAGAGACGAGCGGCCACTACTGTGTGAGATTCAAGTCCATCT 541
DB 1163 TTCACAGAGCGCTGAAGCTGAAGAGACGAGCGGCCACTACTGTGTGAGATTCAAGTCCATCT 544
QY 542 ACATGGCCCAAGAAAGCCCGTGCAGCTGCGCGGTACTTACTAGTGAACACCAAGCTGAGANA 601
DB 1223 ACATGGCCCAAGAAAGCCCGTGCAGCTGCGCGGTACTTACTAGTGAACACCAAGCTGAGANA 604
QY 602 TCACCTCCCAACAGAGACTACACCATGTGAGAGAGTACGAGCGCACCGAGGCGCGCC 661
DB 1283 TCACCTCCCAACAGAGACTACACCATGTGAGAGAGTACGAGCGCACCGAGGCGCGCC 664
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QY 662 ACCACTGTCTCTGA 677
| | | | | | | | | |
Db 1343 ACCACTGTCTCTGA 1358

Search completed: May 29, 2005, 23:53:07
Job time : 549.658 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 29, 2005, 20:02:31 ; Search time 148.77 Seconds
(without alignments)
7193.137 Million cell updates/sec

Title: US-10-081-864A-23

Perfect score: 654

Sequence: 1 gagggcaccggaacgcca.....ccaagctggccacaactga 654

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents NA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	295.6	45.2	723	4 US-10-152-296-1	Sequence 1, Appl
2	224.6	34.3	720	4 US-09-839-650-1	Sequence 1, Appl
3	223	34.1	1482	4 US-09-977-897-1	Sequence 1, Appl
4	167	25.5	801	3 US-09-459-956-7	Sequence 7, Appl
5	152.8	23.4	699	3 US-09-459-956-5	Sequence 5, Appl
6	151.4	23.1	678	3 US-09-459-956-6	Sequence 6, Appl
7	122.8	18.8	690	3 US-09-459-956-2	Sequence 2, Appl
8	110.6	16.9	717	4 US-09-486-241-31	Sequence 31, Appl
9	105.8	16.2	762	1 US-08-532-390-40	Sequence 40, Appl
10	105.8	16.2	762	1 US-08-717-294-40	Sequence 40, Appl
11	105	16.1	1104	3 US-09-277-716-30	Sequence 30, Appl
12	105	16.1	1104	3 US-09-609-1618-30	Sequence 30, Appl
13	105	16.1	1279	3 US-09-277-716-31	Sequence 31, Appl
14	105	16.1	1279	3 US-09-609-1618-31	Sequence 31, Appl
15	104.2	15.9	6355	4 US-09-811-361-2	Sequence 1, Appl
16	104.2	15.9	7353	4 US-08-786-531B-1	Sequence 7, Appl
17	103.8	15.9	1971	2 US-08-818-253-7	Sequence 7, Appl
18	103.8	15.9	1971	2 US-08-818-252-7	Sequence 7, Appl
19	103	15.7	1350	4 US-09-863-901-9	Sequence 10, Appl
20	103	15.7	1404	4 US-09-863-901-10	Sequence 10, Appl
21	103	15.7	1431	4 US-09-863-901-11	Sequence 11, Appl
22	103	15.7	2673	4 US-09-863-901-8	Sequence 12, Appl
23	103	15.7	2718	4 US-09-863-901-12	Sequence 12, Appl
24	103	15.7	3973	4 US-09-863-901-7	Sequence 45, Appl
25	102.6	15.7	717	3 US-09-513-783A-45	Sequence 45, Appl
26	102.6	15.7	717	4 US-09-430-656-45	Sequence 1, Appl
27	102.6	15.7	717	4 US-09-989-025A-1	Sequence 1, Appl

28	102.6	15.7	720	3 US-09-172-063-11	Sequence 11, Appl
29	102.6	15.7	720	3 US-09-172-063-14	Sequence 14, Appl
30	102.6	15.7	720	3 US-09-172-063-18	Sequence 18, Appl
31	102.6	15.7	720	3 US-09-459-956-1	Sequence 1, Appl
32	102.6	15.7	720	3 US-09-316-919-12	Sequence 12, Appl
33	102.6	15.7	720	3 US-09-316-919-15	Sequence 15, Appl
34	102.6	15.7	720	3 US-09-316-919-19	Sequence 19, Appl
35	102.6	15.7	720	4 US-09-602-641-11	Sequence 11, Appl
36	102.6	15.7	720	4 US-09-602-641-14	Sequence 14, Appl
37	102.6	15.7	720	4 US-09-602-641-18	Sequence 18, Appl
38	102.6	15.7	720	4 US-09-920-922-1	Sequence 1, Appl
39	102.6	15.7	720	4 US-09-316-920A-12	Sequence 12, Appl
40	102.6	15.7	720	4 US-09-316-920A-15	Sequence 15, Appl
41	102.6	15.7	720	4 US-09-316-920A-19	Sequence 19, Appl
42	102.6	15.7	761	4 US-09-869-588-25	Sequence 25, Appl
43	102.6	15.7	768	3 US-09-172-063-34	Sequence 34, Appl
44	102.6	15.7	768	4 US-09-602-641-34	Sequence 34, Appl
45	102.6	15.7	850	3 US-09-062-102-2	Sequence 2, Appl

ALIGNMENTS

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RESULT 1
US-10-152-296-1
; Sequence 1, Application US/10152296
; Patent No. 6723537
; GENERAL INFORMATION:
; APPLICANT: Peelle, Beau
; TITLE OF INVENTION: Directed Evolution of Protein in Mammalian Cells
; FILE REFERENCE: 021044-000110US
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US 60/291,871
; PRIOR FILING DATE: 2001-05-18
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 723
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:mammalian
; OTHER INFORMATION: codon-optimized variant (DERED) of Discosoma sp.
; OTHER INFORMATION: "red" red fluorescent protein (RFP)
; NAME/KEY: CDS
; LOCATION: (1)..(723)
; OTHER INFORMATION: DEREDED
US-10-152-296-1
Query Match      45.2%; Score 295.6; DB 4; Length 723;
Best Local Similarity 68.8%; Pred. No. 6.6e-53;
Matches 425; Conservative 0; Mismatches 184; Indels 9; Gaps 1;

QY      1 GAGGGCACCCTGAAGAGCGGCACTTCAAGTCCACCGGCAAGGGGCAACCCCTTC 60
DB      58 GAGGGCACCCTGAAGAGCGGCACTTCAAGTCCACCGGCAAGGGGCAACCCCTTC 117
QY      61 GAGGGCACCCTGAAGAGCGGCACTTCAAGTCCACCGGCAAGGGGCAACCCCTTC 120
DB      118 GAGGGCACCCTGAAGAGCGGCACTTCAAGTCCACCGGCAAGGGGCAACCCCTTC 177
QY      121 GAGGGCACCCTGAAGAGCGGCACTTCAAGTCCACCGGCAAGGGGCAACCCCTTC 180
DB      178 GAGGGCACCCTGAAGAGCGGCACTTCAAGTCCACCGGCAAGGGGCAACCCCTTC 237
QY      181 ATCCCGACTTAAAGAGCGGCACTTCAAGTCCACCGGCAAGGGGCAACCCCTTC 240
DB      238 ATCCCGACTTAAAGAGCGGCACTTCAAGTCCACCGGCAAGGGGCAACCCCTTC 297
QY      241 TAGAGGACGGGCGCTTCTGACCGCCACGAGACACTCTCCGTGACGCGACTGCTCG 300
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Db 298 TTGGAGACGGGGGTGGTGAACCGTGAACCGAGATCTCTCCCTGAGSAGCGCTGCTTC 357
 QY 301 GTGTCAAGGTGAAGATCTCTGGGCAACAACTTCCCGCGGACGGCCCCGTGTATGCAAGAC 360
 Db 358 ATCTCAAGGTGAAGTTCATCGCGGTGAATCTTCCCTCGAGCGGCCCTTAATGAGGAG 417
 QY 361 AAGGCGGCGCCGTGGGAGGCCCTCCACCGAGATCTGTACGAGGTGACGGCGTCTGCGCC 420
 Db 418 AAGACCATGAGGCTGGAGGCGCTTCACCGAGCGCTGTATCCCCGACGCGCTGTGTAAG 477
 QY 421 GGCCAGTCCAGCATGAGCCCTGAGTGCCTCCGCGCGGTGCACCTGACTGCGCACCTGCAC 480
 Db 478 GGCGAGATTCACAAAGGCCCTGAAGGTGAAGAGAGGCGGCATCTACTGTGAGATTCAAG 537
 QY 481 ACCACTTACCGCTCCAAAGAGCGCCCTCCGCGCTGAGATGCTCCGGCTTCCACTTCCAG 540
 Db 538 AGTACTCTACATGGCCCAAGAGGCCG-----TGCACCTCCCGGCTACTACTACACGG 588
 QY 541 GACCAACCCCATGAGATCCTTGAGGAGGTGAGAGGGGCAATGTCTCAACAGAGTACAG 600
 Db 589 GACTCTAAGCTGAGATCACTCCCAACAAGAGACTACACATCTGTGAGAGCATGACGAG 648
 QY 601 GCCGCCGTGGGCGCGCTAC 618
 Db 649 CGCACCGAGGGCGCTGCCAC 666

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RESULT 2
US-09-839-650-1
; Sequence 1, Application US/09839650
; Patent No. 6645761
; GENERAL INFORMATION:
; APPLICANT: Stratagene
; TITLE OF INVENTION: Humanized Polynucleotide Sequence Encoding Renilla Mulleri Green
; Patent No. 6645761
; TITLE OF INVENTION: Fluorescent Protein
; FILE REFERENCE: 25436/1755
; CURRENT APPLICATION NUMBER: US/09/839,650
; CURRENT FILING DATE: 2001-04-19
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Artificial Sequence
FEATURE:
; OTHER INFORMATION: Humanized R. mulleri polynucleotide
NAME/KEY: misc_feature
LOCATION: (1)..(720)
; OTHER INFORMATION: Humanized DNA sequence
US-09-839-650-1

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Query Match	34.3%;	Score 224.6;	DB 4;	Length 720;
Best Local Similarity	62.8%;	Pred. No. 4.5e-38;		
Matches 385; Conservative	0;	Mismatches 219;	Indels 9;	Gaps 2

Qy	1	GAGGGCAACCGGAAACGGCCACTACTTCAAGTGCACCCGGAGAGGGGCAACCCCTTC	60
Db	67	GAGGGCACTCGTGAAACAAACCCGTGTTCACATGAGAGCGTGCAGCAAGGGCAACATCCCG	126
Qy	61	GAGGGCAACCCAGAGATGATGAGGTGATCGAGGGCGGCCCTCGCCCTTCGCGCTTC	120
Db	127	TTCCGCAACCAAGCTGTGTGATCCGCGTGAACAAAGGAGGCCCTTCGCTTCCTTCGCTTC	186
Qy	121	CACATCTCTGCACCTCTCTGATGATCGAGCTTCAAGGCTTCATCAAGTACGTGTCCGAC	180
Db	187	GACATCTGAGAGCCCGCTTCAAGTACGAGCAACGCACTTTCACCAAGTACCCCAACGAC	246
Qy	181	ATCCCCGACTACTTCAGCAAGTCCCTCCCGAGGGCTTCACTTGGAGAGCGACCAACAC	240
Db	247	ATACGCGACTACTTCATCCAGAGCTTCCCGCGCGCTTCATGTACGAGCGCAACCTTGGCG	306

QY 241 TACGAGAGCGGCGCTTCTCTGACCGCCACACAGACACTCTCCTGAGCGGCGACTGCGCT 300

Db 307 TACCGAGACGGGCGGCTGGTGGAGATCCGCACGCACATCACTGAATCAGGACAAAGTTTC 366

QY 301 GTGTACAAAGGTAGATCCTGGGACCAACTTCCCGCGACCGGCCCCGTGATGCAAGAC 360

Db 367 GTGTACCGCGTGGAGTACAGGGACAGCACTTCCCGACGAGCGCCCCGTGATGCAAGAG 426

QY 361 AAGCCCGGCGCGCTGGAGCGCTTCACCGAGATCGTGTACGAGGTGACGGCGTGTGGCC 420

Db 427 ACCATCTGGGCGATGAGCCGACGCTTCGAGGCCCATGTACATGAACACGGCGGTGGTG 486

QY 421 GGCCAGTCCAGATGCGCCCTGAGATGCCCCCGCGCTGCGACACTGACTGACCTGCAC 480

Db 487 GGCAGGTGATCTCTGTGTATCAAGCTGAAACACCGGCAAGTACTACGCTGCGCACATGAAG 546

QY 481 ACCACTACCGGTCCAGGAAGCGCGCTCCGCGCTTCAGAGATCGCGGCTTCCACTTCGAG 540

Db 547 AC-----CTGATAGAGACAGGAGCGGTGTGAAGAGATTTCCCTCTTACCACTTCATC 600

QY 541 GACCAACCGCATCGAGATCCTGGAGAGGTGAGAAAGGCAGATGTCTACAGACGTACGAG 600

Db 601 CAGCAACGCGCTGAGAA---AGACCTACGTGGAGGACGCGGCTTGTGTGAGACGACGAG 657

QY 601 GCCGCGGTGGGC 613

Db 658 ACCGCGCATGCGCC 670

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RESULT 3
US-09-977-897-1
; Sequence 1, Application US/09977897
; Patent No. 6780974
; GENERAL INFORMATION:
; APPLICANT: Chen, Yih-Tai
; TITLE OF INVENTION: A synthetic DNA encoding an orange seapen-derived green fluorescence
; FILE REFERENCE: 41856-5
; CURRENT APPLICATION NUMBER: US/09/977,897
; CURRENT FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1482
; TYPE: DNA
; ORGANISM: Ptilosarcus gurneyi
US-09-977-897-1

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Query Match	34.1%	Score 223;	DB 4;	Length 1482;
Best Local Similarity	62.6%;	Pred. No. 1.1e-37;		
Matches 384; Conservative	0;	Mismatches 220;	Indels 9;	Gaps 2;

QY	1	GAGGGCAACCGTGAACGGGCATCTACTTCAAGTGCACCCGGCAAGGGGAGAGGGCAACCCCTTC	60
Db	79	GAGGGCACTCGGAACAAACCCAGTGTTCAGCATGAGGGCTTCGGCAAGGGCAACGTGCTG	138
QY	61	GAGGGCAACCCAGAGATGAAGATCGAGGTGATCGAGGGCGGCCCTCGCTTCGTGGCTTC	120
Db	139	TTCCGGCAACCAAGCTGATGTCAGATCCGGGTGACAAAGGGGGGCGCTGTGCTTCGTGGCTTC	198
QY	121	CACATCTCTGTCACTCTCTGCAATGTAAGGGCTTCAAAGGCTTCATCAATGATCGTGTCCGG	180
Db	199	GACATCGGAGCAATCGCTTCCAGTACGGCAACCGAGCTTCACCAAGTATCCGACGAC	258
QY	181	ATCCCCGACTACTTCAAGCAGTCCCTCCCGAGGGCTTCACCTGGGAAGGCAACCAAC	240
Db	259	ATCCCCGACTACTTCTGTGAGAGCTTCCCTCGGGCTTCCTTACGAGGAGAACTCGGG	318
QY	241	TACGAGACGGCGGCTTCTTCAACGCGCCACCAAGACACTCTCCCTTGAACGGCGCATGCTCG	300
Db	319	TTCCGAGACGGCGGCATCTGTGAACATCCGAGCGCAATCAGCTCTGAGAGACCAACAATTC	378

QY 301 GTGTCAAGAGTGAAGATCTCTGGCAACAACATTTCCCGCCGAGCCGCTGTATGACGAAC 360
DB 379 CACTACAGAGTGAAGATCCCGGCAACAACATTTCCCGCCGAGCCGCTGTATGACGAAC 438
QY 361 AAGGCGGCGCTGGAGAGCCCTCCACCGAGATCTGTATGAGAGTGAAGCGGCGTGTGCGC 420
DB 439 GCGATCTGTGGGATGAGAGCCGAGCTTCGAGGTGTGTATGATGAACAGCGGCGTGTGCG 498
QY 421 GCGGATCTGAGATGAGCGCTGTGAGAGCCCGGCGTGTGCGCACTGACCTGCACTGCGC 480
DB 499 GCGGATCTGAGATGAGCGCTGTGAGAGCCCGGCGTGTGCGCACTGACCTGCACTGCGC 558
QY 481 ACCACCTACCGCTCCCAAGAGCCCGCTGCGCTGTGAGAGCCCGCTGTGAGAGCCCGCT 540
DB 559 ACCCTTACCGGAG 612
QY 541 GACCAACCGCATGAGATCTCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
DB 613 GACCAACCGCATGAG 669
QY 601 GCGGCGGCTGGGCGC 613
DB 670 ACCGCGATGCGCC 682

RESULT 4
US-09-459-956-7
; Sequence 7, Application US/09459956
; Patent No. 6342379
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Gonzalez, Ili, Jesus E.
; TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY
; FILE REFERENCE: REGEN1290-4
; CURRENT APPLICATION NUMBER: US/09/459,956
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 08/765,860
; PRIOR FILING DATE: 1999-05-08
; PRIOR APPLICATION NUMBER: 08/481,977
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: PCT/US96/09652
; PRIOR FILING DATE: 1996-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 801
; TYPE: DNA
; ORGANISM: *Clavularia* sp
US-09-459-956-7

Query Match 25.5%; Score 167; DB 3; Length 801;
Best Local Similarity 55.7%; Pred. No. 5e-26;
Matches 345; Conservative 0; Mismatches 265; Indels 9; Gaps 1;
QY 1 GAGGCGACCGTGAAGCGCCACTACTTCAAGTGCACCGGAGAGGCGAGGCGCAACCCCTTC 60
DB 169 GAGGAGAAATGTAAACGGGATGCTTTTGTATGAGAAAGAGAGAGAGAGAGAGAGAGAG 228
QY 61 GAGGCGACCGGAGAGATGAGATGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
DB 229 GATGGGACACACACTTTAACTCGAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 288
QY 121 CACATCTGTCTCACTCTGCAATGTAAGGCTCCAGGCTTCAATCAAGTACGTGTCCGCG 180
DB 289 GATATCTGTCTCAAGCGCTTCAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 348
QY 181 ATCCCGAGTACTTGAAG 240
DB 349 ATAGCAAGATATTTCAAG 408
QY 241 TAG 300

DB 409 TTTGAAGCAAAAGGATTTGCAAAAGTGAAGAGATGAGATGAGAGAGAGAGAGAGAG 468
QY 301 GTGTCAAGAGTGAAGATCTCTGGCAACAACATTTCCCGCCGAGCCGCTGTATGACGAAC 360
DB 469 ATCTATGAAGATTTGTTTGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 528
QY 361 AAGGCGGCGCTGGAGAGCCCTCCACCGAGATCTGTATGAGAGTGAAGCGGCGTGTGCGC 420
DB 529 AAAATTTGAAGTGAAG 588
QY 421 GCGGATCTGAGATGAGCGCTGTGAGAGCCCGGCGTGTGCGCACTGACCTGCACTGCGC 480
DB 589 GGAAGATATTAAGCATTTCTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 648
QY 481 ACCACCTACCGCTCCCAAGAGCCCGCTGCGCTGTGAGAGAGAGAGAGAGAGAGAGAG 540
DB 649 AGTATTTCAAG 699
QY 541 GACCAACCGCATGAGATCTCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
DB 700 GACCAACCGCATGAGATCTCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 759
QY 601 GCGGCGGCTGGGCGCTACT 619
DB 760 AATGCAAGTTGCTCGCTATT 778

RESULT 5
US-09-459-956-5
; Sequence 5, Application US/09459956
; Patent No. 6342379
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Gonzalez, Ili, Jesus E.
; TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY
; FILE REFERENCE: REGEN1290-4
; CURRENT APPLICATION NUMBER: US/09/459,956
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 08/765,860
; PRIOR FILING DATE: 1999-05-08
; PRIOR APPLICATION NUMBER: 08/481,977
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: PCT/US96/09652
; PRIOR FILING DATE: 1996-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 699
; TYPE: DNA
; ORGANISM: *Discosoma striata*
US-09-459-956-5

Query Match 23.4%; Score 152.8; DB 3; Length 699;
Best Local Similarity 54.2%; Pred. No. 4.5e-23;
Matches 335; Conservative 0; Mismatches 277; Indels 6; Gaps 1;
QY 1 GAGGCGACCGTGAAGCGCCACTACTTCAAGTGCACCGGAGAGGCGAGGCGCAACCCCTTC 60
DB 55 GAGGAGAAATGTAAACGGGATGCTTTTGTATGAGAAAGAGAGAGAGAGAGAGAGAGAG 114
QY 61 GAGGCGACCGGAGAGATGAGATGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
DB 115 GAGGAGAAATGTAAACGGGATGCTTTTGTATGAGAAAGAGAGAGAGAGAGAGAGAGAG 174
QY 121 CACATCTGTCTCACTCTGCAATGTAAGGCTCCAGGCTTCAATCAAGTACGTGTCCGCG 180
DB 175 CATATTTGTGCGCAATTTCAATGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 234
QY 181 ATCCCGAGTACTTGAAG 240
DB 235 ATACATGATATTTCAAG 294

Query Match	23.1%	Score 151.4	DB 3	length 678
Best Local Similarity	56.2%	Pred. No. 8,8e-23		
Matches	284	Conservative	0	Mismatches 221; Indels 0; Gaps 0

QY	1	GAGGACCGTGAAACGCGCACTACTTCAAGTGCACCGGCAAGGGCGAGGGCAACCCCTTC	60
Db	55	GAAGGAAACGGTCAATAGGGCACAGTTTAAATAGAAAGCGAAGGAGAGGGGCGCATATAC	114
QY	61	GAGGGACACCCAGAGATGAAGTCAGGTGATCGAGGGCGGGCCCTCCCTTCGCTTTC	120
Db	115	GAAGGCCCAATACCGTAAAGTTAAGTTAACCAAGGGGGGACCTTTGCATTTGCTTGG	174
QY	121	CACATCTGTCAACCTCCTGCATGTACGGCTTCCAAAGGCTTCATCAAGTGTGTCTCGGC	180
Db	175	GATATTTTGTACCAACCAATTTCAAGTATGAAAGCAAGGATATATGTAAACACACCTTCGCAC	234
QY	181	ATCCCGCACTACTCAAGCAGTCCCTCCCGAGGGACTTCACCTGGAGACGCACCAAC	240

	Query Match	Similarity	18.8%	Score 122.8	DB 3	Length 690
	Best Local	Similarity	15.6%	Pred. No. 8.4e-17		
	Matches	Conservative	0	Mismatches 277	Indels 15	Gaps 2
QY	1	GAGGGCAACCGTGAACGGCCACTACTTCAAGTGCACCGGCAAGGGCGAGGGCAACCCCTCC	60			
DB	55	GATGGCTGTGCAATAGGGCACTTACTTTCACGTCAAAGGTGAAGGCMAAGGGAAAGCCATAC	114			
QY	61	GAGGGCAACCA-----GGAGTAGAAGATCGAGGATCGAGGGGGCCCCCTGCCCTTC	114			
DB	115	GAGGGAGCGCAGACTTTCGACTTTTAAAGTCAACATGGCCMAAGGGTGGGCCCTTTCGATTC	174			
QY	115	GCCTTCCACATCTGTGCCACTCTCGACGTACAGGGCTCAAGGCTTCAATCAAGTACGTG	174			
DB	175	TCTTTTGACATACATATCAACAGTGTTCMAAATATGGAATTCATGCTTTATCGCATATCT	234			
QY	175	TCCGGCATCCCGGACTATTCGAAGAGTCCCTCCCGAGGGCTTACCTGGGAGGGACAC	234			
DB	235	ACCGATATGCCGAGCTATTTCAACACAGCATTTTCTGACGGAATTCATATGAAGAGACT	294			
QY	235	ACCAACTTACGAGAGACGGCGGCTTCTGTGACGCCCAACAGACACCTCTCTGGACGGCAAC	294			
DB	295	TTTACCTATGAAATGAGAGAGTGTCTACACACCTGGGAATTAAGCTTTAAAGGCAC	354			

Oy 295 TGCCTGGTGTACAAGGTGAAGATCTCTGGCAACAATTCCCGCCGACGCGCCGTATG 354
 Db 355 TGCCTTGAACAATAATCCAGCTTTCTATGAGAGAACTTTCTCGCTGATGACCTGTATG 414
 Oy 355 CAGAACAAAGCCCGCGCTGTGGAGCCCTTCACCGAGATCTGTACGAGGTGAACGCGGTG 414
 Db 415 GCGAAGAAGACAACGTGGTGGGACCATCTTTTGAAGAAAATGACTGTCTGGATGATA 474
 Oy 415 CTGCGCGGCGCAGTCCAGCAATGGCCTTGAAGTSCCCCGCGGTGCGCACTGAACCTGCCAC 474
 Db 475 TTGAAGGTGATATCTCACCGCGTTCTTCATGCTGCAGGAGGTGGCAATTACAGATGCCAA 534
 Oy 475 CTGCAACAACAACCTAACCGCTCCAAAGAGCCCGCGCTCGGCGCTGAAGTSCCGCGTTCCAC 534
 Db 535 TTCCACACTTCTTACAGAACAAAAAAACCGG-----TGACATATCCACCAACCAT 585
 Oy 535 TTGAGAGACCAACGCATTCAGATCTTGAGAGAGGTGAGAAAGGCAAGTCTTACAACAG 594
 Db 586 GTGTGTGAAACATATGCCATTGGGAGGACCGCACTTGAACAAAGGTGGCAACAGTGTTCAGCTG 645
 Oy 595 TACGAGGCTGCGCTGG 610
 Db 646 ACGAGACGACGCTGTTG 661

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RESULT 8
US-09-486-241-31
; Sequence 31, Application US/09486241
; Patent No. 6472184
; GENERAL INFORMATION:
; APPLICANT: Hegemann, Peter
; TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEIC ACID
; TITLE OF INVENTION: POLYMERS
; FILE REFERENCE: 3910/05706
; CURRENT APPLICATION NUMBER: US/09/486,241
; CURRENT FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: PCT/Ep98/05219
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: DE19736591.4
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 31
; LENGTH: 717
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Modified gene from Aquorea victoria
US-09-486-241-31

Query Match          16.9%; Score 110.6; DB 4; Length 717;
Best Local Similarity 52.5%; Pred. No. 3e-14;
Matches 342; Conservative 0; Mismatches 294; Indels 15; Gaps 4

Db      1 GAGGCGACCGTGAACGGCGCACTACTTCAAGTGCACCGGGAAGGGCGAAGGCAACCCCTTC 60
        55 GAGCGCGACGTGAACCGGCACCAAGTTCTCGGTCTCGGGAAGGTGAAGGTGACCGCCACC 114
        61 GAGGCGACCCAGAGATGAAGATCGATGAGTGAAGGGCGGCCCTTGCCTTCGCTTC 120
        115 TACGCGCAGCTGACCCCTGAAGTTCACTGACACAC---CGGCGAAGCTGCGCCGGCCCTGG 171
        121 CACATCCCTGTCCACCTCCCTGCAGATGAAGTACGGGCTCCAAAGCCCTTATCAAGTACGTGTCGGG 180
        172 CCGACCGCTGTGTACCACTTACCTTACCTTACGGGTGTCAGATGCTTCTCCGCGCTACCCGACAC 231
        181 AT-----CCCGACTACTTTCAGACGATCCCTCCCGAAGGCTTTCACCTGGAGCGCAC 234
        223 ATGAAGACACAGACGACTTCTTGAAGTCCGCGCATGCCGAGGGCTTACGTGACGAGAGCGCAC 291
        235 ACCACTTACGAGAGCGGCGGCTTCTGACCGCCACCAAGACACTTCCCTGACCGCGAC 294
        292 ATCTTCTTACAGGACCAACGCACTTACAGACCCGCGCGAGGTCAAGTTGAGGGCGAC 351

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QY 295 TGCCTGCTGTAAACAAGTGAAGATCCTGGGCAACAATCTCCCGCGACGGCCCGGTATG 354

Db 352 ACCCTGTATAACCGCATGAGCTGAAGGCATTCGATTTCAAGAGAGACGGCCACATCTCG 411

QY 355 CAGAACAAAGCCGCGCTGGAGCCCTCAACGAGATCGTGTACGAGTGAACGCGGTG 414

Db 412 GGGCAACAACCTG6---AGTAAACATCAAACTCCCAACAGTGTACATCATGGCCGCAAG 468

QY 415 CTGCGCGGCGCATGTCCAGCATGGCCCTGGAGTGGCCCGCGATCGCCACCTGACTTGCAC 474

Db 469 CAGAAAGACGGATCAAGGTGAATTTCAAGATTC---GCCAACAATCGAGACGGCTCC 525

QY 475 CTGCAACAACCTTACCGCTCCAAAGAGCCCGCTTCGCGCTGAAGATGCCCGCTTCAC 534

Db 526 GTTCAACTGTGGCCGACCACTACCAAGAGAAACCCCATGGCGATGGCCCGCTGTCTG 585

QY 535 TTGAGAGACCAACCGCATCGAGATCTCTGAGAGAGGTGAGAGGGCAAGTGTACAAAGCAG 594

Db 586 CCCGACAACCACTACTGTCCACCCAGTTCGCGCTGTCAAGAGACCCCAAGAGAGCGC 645

QY 595 TACGAGGACCGCGTGGGCGCTTACTTGACAGCGCCGCGCTTCAAAGCTGGCG 645

Db 646 GACCACATGTCTCTGTGAGATTTCATCAACCGTGGCGCATCACCAACGGG 696

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RESULT 9
US-08-532-390-40
; Sequence 40, Application US/08532390
; Patent No. 5795737
; GENERAL INFORMATION:
; APPLICANT: SEED, BRIAN
; APPLICANT: HAAS, JURGEN
; TITLE OF INVENTION: High Level Expression of Proteins
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/532.390
; FILING DATE: 22-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/324.243
; FILING DATE: 19-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: LECH, KAREN P.
; REGISTRATION NUMBER: 35,238
; REFERENCE/DOCKET NUMBER: 00786/294001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 762 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-532-390-40

Query Match      16.2%   Score 105.8; DB 1; Length 762;
Best Local Similarity 52.1%;   Pred. No. 3e-13;
Matches 339; Conservative 0; Mismatches 297; Indels 15; Gaps 4

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QY      1 GAGGGACCGGTGAACGGCCACTACTTCAAGTGACACCGGCAAGGGGCAACCCCTTC 60
DB      85 GACGGGACGTGAACGGCCCAAGTTTCAAGCTGTCCGGGAGGGGCGATGGCAC 144
QY      61 GAGGGACCGGTGAACGGCCACTACTTCAAGTGACACCGGCAAGGGGCAACCCCTTC 120
DB      145 TACGGCAAGCTGACCTGAAAGTTTCAATCTGCAACAC---CGGCAAGCTGCGCTGCGCTG 201
QY      121 CACATCTGTGTCACTCTCTGCAATGTCAGGCTCCAAAGGCTTTATCAAGTGTCTCGGAC 180
DB      202 CCCACCTCTGTGACCACTTCAAGCTGCAAGGCTGCAAGTGTTCAGCGCTTACCCGACAC 261
QY      181 AT-----CCCCGACTACTTCAAGGAGTCCCTCCCGAGGGGCTTCACTCGGAGCGCAC 234
DB      262 ATGAAGACGACACGACTTCTTCAAGTCCGCTATGCTCCGAGGCTTACGACGAGCGCAC 321
QY      235 ACCACCTTACGAGACGGCGGCTTCTGACCGGCAACGAGACACTCCCTGAGACGGCGAC 294
DB      322 ATCTTCTTCAAGGACGACGGCAACTTCAAGACCCGGCGGAGGTGAGTTCAGAGGCGAC 381
QY      295 TGCCTGTGTACAAAGTGAAGTCTTGGGCAACTTCCCGCGGACGCGCCGCTGTATG 354
DB      382 ACCCTGTGAACCGCATGCAAGCTGAAGGCGCATGACTTCAAGAGACGAGCAACATCTCG 441
QY      355 CAGAACAGGCGCGGCGCTGGAGGCTTCAACGAGATGTGTGACAGGTGAGCGCGTG 414
DB      442 GGGGCAAGCTG---AGTACAATCAACAGACGACACAGCTTATATATATGCGGCAAG 498
QY      415 CTGCGCGGCGAGTCCAGCATGCGCTGTGAGTGCCCGCGGCTGCGCACCTGACCTGCAC 474
DB      499 CAGAACAGGCGCATCAAGTGAAGTTTCAAGATCC---GCCAACATCAAGAGCGGCGAC 555
QY      475 CTGACACACCACTACCGCTCCCAAGAGCCCGCTTCCGCTGAGATGCGGCTTCCAC 534
DB      556 GTGAGCTGCGGACCACTACCAAGACACCCCTCATGCGAGCGGCGCTGTGCTG 615
QY      535 TTGCGAGACCAACCGCATGAGTCTTGGAGAGGTGAGAGGCGCAAGTGTACACAG 594
DB      616 CCGGCAACCACTACCTGAGACACCAATGCGGCTGAGACCAAGACCCCAAGAGAGCG 675
QY      595 TACGAGCGCGCGTGGCGGCTACTGCGACCGCGGCGGCTTCCAGCTGAGG 645
DB      676 GATCAGATGTCTGTGAGTGTGAGTGTGACCGCGCGGAGTCACTACGCG 726

RESULT 10
US-08-717-294-40
; Sequence 40, Application US/08717294
; Patent No. 6114148
; GENERAL INFORMATION:
; APPLICANT: SEED, BRIAN
; APPLICANT: HAAS, JURGEN
; TITLE OF INVENTION: HIGH LEVEL EXPRESSION OF
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Ribling LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/717,294
; FILING DATE: 20-SEP-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

```

```

; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Eibling, Karen L.
; REGISTRATION NUMBER: 35,238
; REFERENCE/DOCKET NUMBER: 00786/345001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-428-0200
; TELEFAX: 617-428-7045
;
; TELEK:
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 762 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other
; US-08-717-294-40

Query Match      16.2%; Score 105.8; DB 3; Length 762;
Best Local Similarity 52.1%; Pred. No. 3e-13;
Matches 339; Conservative 0; Mismatches 297; Indels 15; Gaps 4;

QY      1 GAGGGACCGGTGAACGGCCACTACTTCAAGTGACACCGGCAAGGGGCAACCCCTTC 60
DB      85 GACGGGACGTGAACGGCCCAAGTTTCAAGCTGTCCGGGAGGGGCGATGGCAC 144
QY      61 GAGGGACCGGTGAACGGCCACTACTTCAAGTGACACCGGCAAGGGGCAACCCCTTC 120
DB      145 TACGGCAAGCTGACCTGAAAGTTTCAATCTGCAACAC---CGGCAAGCTGCGCTGCGCTG 201
QY      121 CACATCTGTGTCACTCTCTGCAATGTCAGGCTCCAAAGGCTTTATCAAGTGTCTCGGAC 180
DB      202 CCCACCTCTGTGACCACTTCAAGCTGCAAGGCTGCAAGTGTTCAGCGCTTACCCGACAC 261
QY      181 AT-----CCCCGACTACTTCAAGGAGTCCCTCCCGAGGGGCTTCACTCGGAGCGCAC 234
DB      262 ATGAAGACGACACGACTTCTTCAAGTCCGCTATGCTCCGAGGCTTACGACGAGCGCAC 321
QY      235 ACCACCTTACGAGACGGCGGCTTCTGACCGGCAACGAGACACTCCCTGAGAGCGGAC 294
DB      322 ATCTTCTTCAAGGACGACGGCAACTTCAAGACCCCGCGGAGTGAAGTTGAGGGGAC 381
QY      295 TGCCTGTGTACAAAGTGAAGTCTTGGGCAACTTCCCGCGGACGCGCCGCTGTATG 354
DB      382 ACCCTGTGAACCGCATGCAAGCTGAAGGCGATGCACTTCAAGAGACGAGCAATCTCG 441
QY      355 CAGAACAGGCGCGGCGCTGGAGGCTTCAACGAGATGTGTGACAGGTGAGCGGCTG 414
DB      442 GGGGCAAGCTG---AGTACAATCAACAGACGACCAAGCTTATATATATGCGGCAAG 498
QY      415 CTGCGCGGCGAGTCCAGCATGCGCTGTGAGTGCCCGCGGCTGCGCACCTGACTGCGAC 474
DB      499 CAGAACAGGCGCATCAAGTGAAGTTTCAAGATCC---GCCAACATCAAGAGCGGCGAC 555
QY      475 CTGACACACCACTACCGCTCCCAAGAGCCCGCTTCCGCTGAGATGCGGCTTCCAC 534
DB      556 GTGAGCTGCGGACCACTACCAAGACACCCCTCATGCGAGCGGCGCTGTGCTG 615
QY      535 TTGCGAGACCAACCGCATGAGTCTTGGAGAGGTGAGAGGCGCAAGTGTCAACAG 594
DB      616 CCGGCAACCACTACCTGAGACACCAATGCGGCTGAGACCAAGACCCCAAGAGAGCG 675
QY      595 TACGAGCGCGCGTGGCGGCTACTGCGACCGCGGCGGCTTCCAGCTGAGG 645
DB      676 GATCAGATGTCTGTGAGTGTGAGTGTGACCGCGCGGAGTCACTACGCG 726

RESULT 11
US-09-277-716-30
; Sequence 30, Application US/09277716A
; Patent No. 6232107
; GENERAL INFORMATION:

```

```

; APPLICANT: Bryan, Bruce
; APPLICANT: Szent-Gyorgyi, Christopher
; APPLICANT: PROLUME, LTD.
; TITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE
; CURRENT APPLICATION NUMBER: US/09/277,716A
; EARLIER FILING DATE: 1998-03-26
; EARLIER APPLICATION NUMBER: 60/102,939
; EARLIER FILING DATE: 1998-10-01
; EARLIER APPLICATION NUMBER: 60/089,367
; EARLIER FILING DATE: 1998-06-15
; EARLIER APPLICATION NUMBER: 60/079,624
; EARLIER FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 1104
; TYPE: DNA
; ORGANISM: Ptilosarcus gurneyi
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (34)..(747)
; FEATURE:
; OTHER INFORMATION: Ptilosarcus Green Fluorescent Protein (GFP) (Insert A)
US-09-277-716-30
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Query Match      16.1%; Score 105; DB 3; Length 1104;
Best Local Similarity 50.7%; Pred. No. 4.8e-13;
Matches 252; Conservative 0; Mismatches 245; Indels 0; Gaps 0;
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QY      1 GAGGCGACCGTGAAGCGGCACCTACTTCAAGTGCACCGGACGGGAGGAGCAACCCCTC 60
DB      97 GAGGAAATCGTGAACAATACGCTTTTTCATGAGAGATTGGAAAGGCAATGTATTA 156
QY      61 GAGGCGACCGGAGAGATGAATGAGTGAATGAGGCGGCGCCCTGCTTGCCTTC 120
DB      157 TTTGGAACAATGATGATGCAATCGGGTTACAAAGGAGGATCCGTGCAATTCGCTTTC 216
QY      121 CACATCTGTCACCTCTGCGATGACGGCTCCAAAGGCTTTCATCAAGTGTGCGGC 180
DB      217 GATATTGTTTCATAGCTTTCCAAATACGGGAATCGCATTTACGAAATACCCAGACGAC 276
QY      181 ATCCCGACTACTTCAAGCAGTCCCTCCCGAGGGCTTCACTGGAGGCGACACACACC 240
DB      277 ATTGGGACTACTTGTTCATCATATTCGCGGTGATTTTTCAGAAAGAAATCTACGC 336
QY      241 TAAGAGACGGGCGCTTCTGACCGCCACAGACACCTCCCTGAGCGGCGACTGCTG 300
DB      337 TTTGAAGATGGCGCATTTGTGACATTCGTTCAATATTAAGTTAGAGATGATTAAGTTC 396
QY      301 GTGTCAAGGTGAAGATCTGTGGCAACAATTCCTCCCGACGAGCGCCGTGATGCAAGAC 360
DB      397 CACTCAAAAGTGAATATAGAGCAACGGTTTCCCTAGTAAGAACCCGTGATGCAAAA 456
QY      361 AAGGCGGCGCGTGGAGGCGCTTCCACCGAGATCGTGTACGAGTGAAGCGGCTGCTGCGC 420
DB      457 GCCATCTCTGGATGAGGCAATCGTTTGAAGTGTCTATACATAAGCGGCGTTTCTGGTG 516
QY      421 GCGCAGTCAGAGTGGCCCTGAGAGTCCCGGCGGTGCGCACCTGACCTGCGACCTGCAC 480
DB      517 GCGGAAGTGAATCTGTTTACAAACTCGAGTCAAGGGAATATTAATCTCGTGCCACATGAAA 576
QY      481 ACCACTTACCGCTCCAA 497
DB      577 ACGTTTACAGATCCAA 593
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RESULT 12
US-09-609-161B-30
; Sequence 30, Application US/09609161B
; Patent No. 6436682
; GENERAL INFORMATION:
; APPLICANT: Bryan, Bruce
; APPLICANT: Szent-Gyorgyi, Christopher
```

```

; APPLICANT: PROLUME, LTD.
; TITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE LUC
; TITLE OF INVENTION: AND FLUORESCENT PROTEINS AND THE USE THEREOF IN DIAGNOSTICS, HT
; FILE REFERENCE: 24729-121B
; CURRENT APPLICATION NUMBER: US/09/609,161B
; EARLIER FILING DATE: 2000-06-30
; EARLIER APPLICATION NUMBER: 09/277,716
; EARLIER FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: 60/102,939
; EARLIER FILING DATE: 1998-10-01
; EARLIER APPLICATION NUMBER: 60/089,367
; EARLIER FILING DATE: 1998-06-15
; EARLIER APPLICATION NUMBER: 60/079,624
; EARLIER FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 1104
; TYPE: DNA
; ORGANISM: Ptilosarcus gurneyi
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (34)..(747)
; OTHER INFORMATION: Ptilosarcus Green Fluorescent Protein (GFP) (Insert A)
US-09-609-161B-30
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Query Match      16.1%; Score 105; DB 3; Length 1104;
Best Local Similarity 50.7%; Pred. No. 4.8e-13;
Matches 252; Conservative 0; Mismatches 245; Indels 0; Gaps 0;
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QY      1 GAGGCGACCGTGAAGCGGCACCTACTTCAAGTGCACCGGACGGGAGGAGCAACCCCTC 60
DB      97 GAGGAAATCGTGAACAATACGCTTTTTCATGAGAGATTGGAAAGGCAATGTATTA 156
QY      61 GAGGCGACCGGAGAGATGAATGAGTGAATGAGGCGGCGCCCTGCTTGCCTTC 120
DB      157 TTTGGAACAATGATGATGCAATCGGGTTACAAAGGAGGATCCGTGCAATTCGCTTTC 216
QY      121 CACATCTGTCACCTCTGCGATGACGGCTCCAAAGGCTTTCATCAAGTGTGCGGC 180
DB      217 GATATTGTTTCATAGCTTTCCAAATACGGGAATCGCATTTACGAAATACCCAGACGAC 276
QY      181 ATCCCGACTACTTCAAGCAGTCCCTCCCGAGGGCTTCACTGGAGGCGACACACACC 240
DB      277 ATTGGGACTACTTGTTCATCATATTCGCGGTGATTTTTCAGAAAGAAATCTACGC 336
QY      241 TAAGAGACGGGCGCTTCTGACCGCCACAGACACCTCCCTGAGCGGCGACTGCTG 300
DB      337 TTTGAAGATGGCGCATTTGTGACATTCGTTCAATATTAAGTTAGAGATGATTAAGTTC 396
QY      301 GTGTCAAGGTGAAGATCTGTGGCAACAATTCCTCCCGACGAGCGCCGTGATGCAAGAC 360
DB      397 CACTCAAAAGTGAATATAGAGCAACGGTTTCCCTAGTAAGAACCCGTGATGCAAAA 456
QY      361 AAGGCGGCGCGTGGAGGCGCTTCCACCGAGATCGTGTACGAGTGAAGCGGCTGCTGCGC 420
DB      457 GCCATCTCTGGATGAGGCAATCGTTTGAAGTGTCTATACATAAGCGGCGTTTCTGGTG 516
QY      421 GCGCAGTCAGAGTGGCCCTGAGAGTCCCGGCGGTGCGCACCTGACCTGCGACCTGCAC 480
DB      517 GCGGAAGTGAATCTGTTTACAAACTCGAGTCAAGGGAATATTAATCTCGTGCCACATGAAA 576
QY      481 ACCACTTACCGCTCCAA 497
DB      577 ACGTTTACAGATCCAA 593
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RESULT 13
US-09-277-716-31
; Sequence 31, Application US/09277716A
; Patent No. 6232107
; GENERAL INFORMATION:
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```

/ APPLICANT: PROLUME, LTD.
/ TITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE LUC
/ TITLE OF INVENTION: AND FLUORESCENT PROTEINS AND THE USE THEREOF IN DIAGNOSTICS, HIGH
/ TITLE OF INVENTION: SCREENING AND NOVELTY ITEMS
/ FILE REFERENCE: 24729-121B
/ CURRENT APPLICATION NUMBER: US/09/609,161B
/ CURRENT FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: 09/277,716
/ PRIOR FILING DATE: 1999-03-26
/ PRIOR APPLICATION NUMBER: 60/102,939
/ PRIOR FILING DATE: 1998-10-01
/ PRIOR APPLICATION NUMBER: 60/089,367
/ PRIOR FILING DATE: 1998-06-15
/ PRIOR APPLICATION NUMBER: 60/079,624
/ PRIOR FILING DATE: 1998-03-27
/ NUMBER OF SEQ ID NOS: 32
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 31
/ LENGTH: 1279
/ TYPE: DNA
/ ORGANISM: Ptilosarcus gurneyi
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (7)..(720)

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Query Match 16.1%; Score 105; DB 3; Length 1279;

	Matched	Conservative	Nonconservative	Mismatches	Indels	Gaps
QY	1	GAGGGCACCGTGAA	CGGCGACCTACTTTCATCAAGTGAC	CCGGGCAAGGGCGAGGCGCAACCCCTCTG	60	
Db	70	GAGGAATTCGGAACAAT	CACGTTTTTTCATGAGAGAGATTGTGAAAAAGGCAATGTATTA	129		
QY	61	GAGGGCACCCGAGAGATG	AAGATGAGGTGATCGAGGGCGGGCCCTGGCCCTTGCCCTTG	120		
Db	130	TTTGGAAACCAATTGATG	CATATTCGGGTTCACAAAGGAGGTCCGTTCACATTCGCTTTC	189		
QY	121	CACATCTGTGCACCTC	CTGCGATGACGGCTCCAAAGCCCTTCATCAAGTACGTGTCGGGC	180		
Db	190	GACATGTGTTCCATAG	CTTTCCAATACGGGAATCGCACTTTCACGAATATCCACAGACGAC	249		
QY	181	ATCCCGGACATCTTCAG	AGATCCCTCCCGGAGGCTTCACCTGGGAGCGACACACACACC	240		
Db	250	ATTGGGACATACCTTG	TTCATCAATTCCTCGCTGGATTTTTCACGAAAGAAATTCATGCG	309		
QY	241	TACGAGGACGGCGGCT	CTTGACCGGCCACGAGACACTTCCCTGAGCGGCGACTGCCGTG	300		
Db	310	TTTGAAAGATGGCGCAT	TGTTGACATTCGTTCAAGATTAAGTTTAAAGATGATTAAGTTC	369		
QY	301	GTTGACAAAGTGAAAG	ATCTGCGGACAACTTCCCGGCCGACGGCCCGGTGATCAGAAC	360		
Db	370	CACATCAAAAGTGAGTA	TAGAGGCAACGGTTTCCCTAGTAAAGCAACCCGATGATCAAAAA	429		
QY	361	AAGGCGGCGCGCTG	GGAGCCCTCCACCGAGATCTGTGACAGGTGAGCGGCGTCTGGCG	420		
Db	430	GCGATCTCGGCATGAG	AGCATGGTTTGAAGGTGTATCAATGAACAGGAGGGCTTCTGGTG	489		
QY	421	GGCGCATTCAGACAT	GCGCCCTGGAAGTCCCGGCGGTGCGCACCTGACCTGACACTTGAC	480		
Db	490	GGCGCAATGATGATC	CGTTTACAAACTGAGTCAAGGAACTTATTACTCGTGGCACATGAAA	549		
QY	481	ACGACCTACCGCTCCA	497			

RESULT 15
US-09-011-361-2
; Sequence 2, Application US/09811361
; Patent No. 6730821
; GENERAL INFORMATION:

APPLICANT: Guenther, Catherine
TITLE OF INVENTION: TRANSGENIC MICE CONTAINING
TITLE OF INVENTION: RETINA-SPECIFIC NUCLEAR RECEPTOR GENE DISRUPTIONS
FILE REFERENCE: R-125
CURRENT APPLICATION NUMBER: US/09/811,361
CURRENT FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: US 60/190,348
PRIOR FILING DATE: 2000-03-16
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 6355
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Phage Vector
US-09-811-361-2

Query Match 15.9%; Score 104.2; DB 4; Length 6355;
Best Local Similarity 51.9%; Pred.No. 9.7e-13;
Matches 338; Conservative 0; Mismatches 298; Indels 15; Gaps 4;

QY 1 GAGGGACCGGTGAACGGCCACTACTTCAAGTGACACGGCAAGGGCGAACCCTTC 60
DB 666 GACGGCGACGTAAACGGCCACAAGTTCAAGCTGTCGGCGAGGGCGAGTCCAC 725
QY 61 GAGGGACCGAGAGATGAAGTGAAGGTGATGAGGGCGGCCCCCTTCGCTTC 120
DB 726 TACGGCAAGTGAACCTGAAGTTCACTGACACAC---CGGCACAGCTGCCCTGCTG 782
QY 121 CACATCCGTGACCTCTGATGATGAGGCTTCAAGGCTTCATCAAGTAAGTCCGGC 180
DB 783 CCACCTCTGTGACACCTGACCTGACCTGACGCTGACGCTTCAAGCTTCAAGCTG 842
QY 181 ATC-----CCGACTACTTCAAGAGATGCTCCCTCCGAGAGGCTTCACTGGAGCGCAC 234
DB 843 ATGAAGCAGCAGACTTCTTCAAGTCCGCGCATGCCGAGAGGCTACGTCAAGAGCGCAC 902
QY 235 ACCACTAGAGAGAGCGGCGCTTCTGACCGGCCACAGACACTCCCTGGAGCGGAC 294
DB 903 ATCTTCTTCAAGGAGCAGCGCAATACAAAGACCCGCGGAGTGAAGTTGAGGGCGAC 962
QY 295 TGCCTGTGTACAGAGTGAAGTCTGGGCAACACTTCCCGCGGACGCGCCGCTGATG 354
DB 963 ACCCTGTGAACCGCATGAGCTGAAGGAGCATGACTTCAAGAGAGAGCGCAACTCTG 1022
QY 355 CAGAACAAAGCCGCGCGCTGGAGGCTTCAACGAGATGTTGTAAGAGTGGAGCGCGTG 414
DB 1023 GGGCAGAGCTGG---AGTACAACTACAAAGCCCAAGCTTATATCATGCGGACAAAG 1079
QY 415 CTGCGCGGCGCAGTCAGATGCGCTGAGATGCCCCGGGCGGTGCGCACTTGCAAC 474
DB 1080 CAGAAAGAACGGCATCAAGGTGAATTTCAAGATCC---GCCACAAATCAGAGACGGCAGC 1136
QY 475 CTGCAACACCTTACCGCTTCAAGAAAGCCGCGCTCGGCTGAGATGCCGCGCTTCCAC 534
DB 1137 GTGACGCTGCGGACCATCTACAGCAACACCCCATGCGGACGCGCCGCTGCTG 1196
QY 535 TTGAGAGCAACCGCATGAGATCTTGAAGAGAGTGAAGAGGCAAGTGTACAGAGCAG 594
DB 1197 CCGGCAACCACTACTAGAGAGCCAGTCCGCGCTGAGCAAAAGACCCCAAGAGAGAGCGC 1256
QY 595 TACGAGCGCGCGTGGCGCGCTACTGCGACGCGCGCCCTTCAAGCTGGGC 645
DB 1257 GATCAGATGCTCTGCTGAGATTCGTGACCGCGCGGAGATCACTCTCGGC 1307

Search completed: May 29, 2005, 21:17:21
Job time : 151.77 sec

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 29, 2005, 21:06:21 ; Search time 526.342 Seconds
(without alignments)
7628.632 Million cell updates/sec

Title: US-10-081-864a-23

Perfect score: 654

Sequence: 1 gagggcaccggaagcga.....ccaagctggccacaactga 654

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5700845 seqs, 3069779757 residues

Total number of hits satisfying chosen parameters: 11401650

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

1:	/cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2:	/cgn2_6/ptodata/2/pubpna/BCT_NEW_PUB.seq:*
3:	/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4:	/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5:	/cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6:	/cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
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8:	/cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9:	/cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
10:	/cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
11:	/cgn2_6/ptodata/2/pubpna/US09C_NEW_PUB.seq:*
12:	/cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
13:	/cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
14:	/cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
15:	/cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
16:	/cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
17:	/cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
18:	/cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
19:	/cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
20:	/cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
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22:	/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	654	100.0	654	US-10-081-864-23	Sequence 23, Appl
2	652.4	99.8	1404	US-10-806-930-7	Sequence 7, Appl
3	649.2	99.3	707	US-10-006-922-39	Sequence 39, Appl
4	649.2	99.3	707	US-10-081-864-21	Sequence 21, Appl
5	647.6	99.0	1398	US-10-806-930-9	Sequence 9, Appl
6	641.2	98.0	699	US-10-006-922-41	Sequence 41, Appl
7	623.8	95.4	696	US-10-724-178-17	Sequence 17, Appl
8	566.6	86.6	591	US-10-724-178-1046	Sequence 1046, Ap
9	487.4	74.5	555	US-10-724-178-1064	Sequence 1064, Ap
10	436.4	66.7	504	US-10-724-178-1060	Sequence 1060, Ap
11	415.8	63.6	696	US-10-006-922-13	Sequence 13, Appl

12	415.8	63.6	696	14	US-10-081-864-9	Sequence 9, Appl
13	412.4	63.1	767	14	US-10-155-809-1	Sequence 1, Appl
14	410.8	62.8	767	14	US-10-155-809-3	Sequence 3, Appl
15	409.2	62.6	767	14	US-10-155-809-5	Sequence 5, Appl
16	398	60.9	456	18	US-10-724-178-1052	Sequence 1052, Ap
17	396.8	60.7	687	9	US-09-976-673-13	Sequence 11, Appl
18	395.2	60.4	687	9	US-09-976-673-13	Sequence 13, Appl
19	395.2	60.4	1396	9	US-09-976-673-15	Sequence 15, Appl
20	395.2	60.4	1396	18	US-10-806-930-1	Sequence 1, Appl
21	395.2	60.4	1424	9	US-09-976-673-17	Sequence 17, Appl
22	395.2	60.4	1424	18	US-10-806-930-3	Sequence 3, Appl
23	382.8	58.5	405	18	US-10-724-178-1050	Sequence 1050, Ap
24	382.8	52.1	363	18	US-10-724-178-1058	Sequence 1058, Ap
25	300.4	45.9	681	14	US-10-121-258-7	Sequence 7, Appl
26	299.6	45.8	675	18	US-10-724-178-15	Sequence 15, Appl
27	299.6	45.8	678	14	US-10-121-258-9	Sequence 9, Appl
28	298.8	45.7	675	13	US-10-006-922-38	Sequence 38, Appl
29	298.8	45.7	675	14	US-10-081-864-3	Sequence 13, Appl
30	298.8	45.7	678	14	US-10-081-864-7	Sequence 7, Appl
31	298.8	45.7	678	16	US-10-315-920-1	Sequence 1, Appl
32	298.8	45.7	747	18	US-10-785-862-10	Sequence 10, Appl
33	298.8	45.7	1050	13	US-10-060-857-7	Sequence 7, Appl
34	298.6	45.7	649	18	US-10-439-262-12	Sequence 12, Appl
35	297.2	45.4	678	13	US-10-006-922-36	Sequence 36, Appl
36	297.2	45.4	678	14	US-10-081-864-14	Sequence 14, Appl
37	297.2	45.4	678	14	US-10-121-258-5	Sequence 5, Appl
38	297.2	45.4	678	16	US-10-315-920-3	Sequence 3, Appl
39	297.2	45.4	678	16	US-10-315-920-5	Sequence 5, Appl
40	297.2	45.4	681	14	US-10-121-258-3	Sequence 3, Appl
41	297.2	45.4	681	14	US-10-121-258-23	Sequence 23, Appl
42	297.2	45.4	1638	15	US-10-214-932-51	Sequence 51, Appl
43	297.2	45.4	1647	15	US-10-214-932-75	Sequence 75, Appl
44	297.2	45.4	4692	15	US-10-161-403-29	Sequence 29, Appl
45	297.2	45.4	4692	18	US-10-433-640-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-10-081-864-23
; Sequence 23, Application US/10081864
; Publication No. US2003002287A1
; GENERAL INFORMATION:
; APPLICANT: Lukyanov, Sergey
; APPLICANT: Lukyanov, Konstantin
; APPLICANT: Yarushevich, Yurly
; APPLICANT: Savitsky, Alexandr
; APPLICANT: Pradkov, Arcady
; TITLE OF INVENTION: No. US2003002287A1 Aggregating Fluorescent Proteins and
; TITLE OF INVENTION: Methods for Using the Same
; FILE REFERENCE: CLON-067
; CURRENT APPLICATION NUMBER: US/10/081,864
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: 10/006,922
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/270,983
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 654
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: non-aggregating mutant
US-10-081-864-23

Query Match 100.0%; Score 654; DB 14; Length 654;
Best Local Similarity 100.0%; Pred. No. 4.6e-154;
Matches 654; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAGGACCGTAGGCGCACTTCAAGTGCACCGGCAAGGCGCAACCCCTTC 60

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Db 1 GAGGGCACCGTGAACGGCACTACTTCAAGTGCACCGGAAAGGGAGGCAACCCCTTC 60
Qy 61 GAGGGCACCGTGAACGGCACTACTTCAAGTGCACCGGAAAGGGAGGCAACCCCTTC 120
Db 61 GAGGGCACCGTGAACGGCACTACTTCAAGTGCACCGGAAAGGGAGGCAACCCCTTC 120
Qy 121 CACATCTGTCACTCTCTGATGTAGAGGCTCCAAAGGCTTCATCAAGTACGTGCGGC 180
Db 121 CACATCTGTCACTCTCTGATGTAGAGGCTTCCTCAAGGCTTCATCAAGTACGTGCGGC 180
Qy 181 ATCCCGACTACTTCAAGCAAGTCCCTCCCGAGGGCTTCACCTGGAAGCGACCAACC 240
Db 181 ATCCCGACTACTTCAAGCAAGTCCCTCCCGAGGGCTTCACCTGGAAGCGACCAACC 240
Qy 241 TACGAGAGCGGCGGCTTCTGACCGGCGCAACGACACTCCCTGGAAGCGGCACTGCGC 300
Db 241 TACGAGAGCGGCGGCTTCTGACCGGCGCAACGACACTCCCTGGAAGCGGCACTGCGC 300
Qy 301 GTGTACAAAGTGAAGATCTGTGGCAACAATTCCCGCGCAAGCGCCCTGTATGAGAAC 360
Db 301 GTGTACAAAGTGAAGATCTGTGGCAACAATTCCCGCGCAAGCGCCCTGTATGAGAAC 360
Qy 361 AAGGCGGCGGCTGTGGAGCCCTTCCACCGAGATGTGTACGAGTGAACGCGGTGCTGCGC 420
Db 361 AAGGCGGCGGCTGTGGAGCCCTTCCACCGAGATGTGTACGAGTGAACGCGGTGCTGCGC 420
Qy 421 GGGCAGTCAAGATGAGCGCTGTGAGTCCCGCGGCTGCGCACTGACCTGCACTGAC 480
Db 421 GGGCAGTCAAGATGAGCGCTGTGAGTCCCGCGGCTGCGCACTGACCTGCACTGAC 480
Qy 481 ACCACCTACCGCTCCCAAGAGCCGCTCCGCGCTGAAGATCCCGGCTTCACCTTCGAG 540
Db 481 ACCACCTACCGCTCCCAAGAGCCGCTCCGCGCTGAAGATCCCGGCTTCACCTTCGAG 540
Qy 541 GACCAACCGCATGAGATCTGTGAGAGGTGAGAAAGGCAAGTGTACAAAGCATGACGAG 600
Db 541 GACCAACCGCATGAGATCTGTGAGAGGTGAGAAAGGCAAGTGTACAAAGCATGACGAG 600
Qy 601 GCCGCGGTGGGCGGCTACTGAGAGCGCGCCCTCCCAAGCTGGGCGCAACATGA 654
Db 601 GCCGCGGTGGGCGGCTACTGAGAGCGCGCCCTCCCAAGCTGGGCGCAACATGA 654
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RESULT 2

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US-10-806-930-7
; Sequence 7, Application US/10806930
; Publication No. US20040216180A1
; GENERAL INFORMATION:
; APPLICANT: Lukyanov, Sergey
; TITLE OF INVENTION: Nucleic Acids Encoding Linked
; FILE REFERENCE: Chromo/Fluorescent Domains and Methods for Using the Same
; CURRENT APPLICATION NUMBER: US/10/806,930
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: 09/976,673
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/356,225
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/383,336
; PRIOR FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: PCT/US02/32560
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1404
; TYPE: DNA
; ORGANISM: anthozoa
US-10-806-930-7
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Query Match 99.8%; Score 652.4; DB 18; Length 1404;
Best Local Similarity 99.8%; Pred. No. 1.2e-153;

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Matches 653; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GAGGGCACCGTGAACGGCACTACTTCAAGTGCACCGGAAAGGGAGGCAACCCCTTC 60
Db 46 GAGGGCACCGTGAACGGCACTACTTCAAGTGCACCGGAAAGGGAGGCAACCCCTTC 105
Qy 61 GAGGGCACCGTGAACGGCACTACTTCAAGTGCACCGGAAAGGGAGGCAACCCCTTC 120
Db 106 GAGGGCACCGTGAACGGCACTACTTCAAGTGCACCGGAAAGGGAGGCAACCCCTTC 165
Qy 121 CACATCTGTCACTCTCTGATGTAGAGGCTCCAAAGGCTTCATCAAGTACGTGCGGC 180
Db 121 CACATCTGTCACTCTCTGATGTAGAGGCTTCCTCAAGGCTTCATCAAGTACGTGCGGC 180
Qy 166 CACATCTGTCACTCTCTGATGTAGAGGCTTCCTCAAGGCTTCATCAAGTACGTGCGGC 225
Db 166 CACATCTGTCACTCTCTGATGTAGAGGCTTCCTCAAGGCTTCATCAAGTACGTGCGGC 225
Qy 181 ATCCCGACTACTTCAAGCAAGTCCCTCCCGAGGGCTTCACCTGGAAGCGACCAACC 240
Db 226 ATCCCGACTACTTCAAGCAAGTCCCTCCCGAGGGCTTCACCTGGAAGCGACCAACC 285
Qy 241 TACGAGAGCGGCGGCTTCTGACCGGCGCAACGACACTCCCTGGAAGCGGCACTGCGC 300
Db 286 TACGAGAGCGGCGGCTTCTGACCGGCGCAACGACACTCCCTGGAAGCGGCACTGCGC 345
Qy 301 GTGTACAAAGTGAAGATCTGTGGCAACAATTCCCGCGCAAGCGCCCTGTATGAGAAC 360
Db 346 GTGTACAAAGTGAAGATCTGTGGCAACAATTCCCGCGCAAGCGCCCTGTATGAGAAC 405
Qy 361 AAGGCGGCGGCTGTGGAGCCCTTCCACCGAGATGTGTACGAGTGAACGCGGTGCTGCGC 420
Db 406 AAGGCGGCGGCTGTGGAGCCCTTCCACCGAGATGTGTACGAGTGAACGCGGTGCTGCGC 465
Qy 421 GGGCAGTCAAGATGAGCGCTGTGAGTCCCGCGGCTGCGCACTGACCTGCACTGAC 480
Db 466 GGGCAGTCAAGATGAGCGCTGTGAGTCCCGCGGCTGCGCACTGACCTGCACTGAC 525
Qy 481 ACCACCTACCGCTCCCAAGAGCCGCTCCGCGCTGAAGATCCCGGCTTCACCTTCGAG 540
Db 526 ACCACCTACCGCTCCCAAGAGCCGCTCCGCGCTGAAGATCCCGGCTTCACCTTCGAG 585
Qy 541 GACCAACCGCATGAGATCTGTGAGAGGTGAGAAAGGCAAGTGTCTCAACAGTACGAG 600
Db 586 GACCAACCGCATGAGATCTGTGAGAGGTGAGAAAGGCAAGTGTCTCAACAGTACGAG 645
Qy 601 GCCGCGGTGGGCGGCTACTGAGAGCGCGCCCTCCCAAGCTGGGCGCAACATGA 654
Db 646 GCCGCGGTGGGCGGCTACTGAGAGCGCGCCCTCCCAAGCTGGGCGCAACATGA 699
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RESULT 3

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US-10-006-922-39
; Sequence 39, Application US/10006922
; Publication No. US20020197676A1
; GENERAL INFORMATION:
; APPLICANT: Lukyanov, Sergey A.
; APPLICANT: Fradkov, Arcady F.
; APPLICANT: Labas, Yulii A.
; APPLICANT: Terekikh, Aleksey
; TITLE OF INVENTION: No. US20020197676A1el Chromophores/Fluorophores and
; FILE REFERENCE: CLON-035C1P
; CURRENT APPLICATION NUMBER: US/10/006,922
; CURRENT FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 09/120,330
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: 09/457,898
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 09/458,144
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 09/458,477
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 09/457,556
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 09/444,338
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; PRIOR FILING DATE: 1999-11-19
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FaSTSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 707
; TYPE: DNA
; ORGANISM: Anemonia sulcata
US-10-006-922-39

Query Match      99.3%; Score 649.2; DB 13; Length 707;
Best Local Similarity 99.5%; Pred. No. 7.3e-153;
Matches 651; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAGGGGACCGGTGAAGGCGCACTACTTCAAGTGACCGGCAAGGGCGAAGGGCAACCCCTTC 60
DB 49 GAGGGGACCGGTGAAGGCGCACTACTTCAAGTGACCGGCAAGGGCGAAGGGCAACCCCTTC 108
QY 61 GAGGGGACCGGTGAAGGCGCACTACTTCAAGTGACCGGCAAGGGCGAAGGGCAACCCCTTC 120
DB 109 GAGGGGACCGGTGAAGGCGCACTACTTCAAGTGACCGGCAAGGGCGAAGGGCAACCCCTTC 168
QY 121 CACATCTGTCCACTCTCTGATGATGAGGCTCCAGGCTTCATCAAGTACGTTCGGGC 180
DB 169 CACATCTGTCCACTCTCTGATGATGAGGCTCCAGGCTTCATCAAGTACGTTCGGGC 228
QY 181 ATCCCGACTACTTCAAGGAGTCCCTCCCGAGGGCTTCACTGGAGGCGCAACCAACC 240
DB 229 ATCCCGACTACTTCAAGGAGTCCCTCCCGAGGGCTTCACTGGAGGCGCAACCAACC 288
QY 241 TACGAGGACGGGCGCTTCTGACCGGCCACAGGACACCTCCCTGAGCGGCACTGCTG 300
DB 289 TACGAGGACGGGCGCTTCTGACCGGCCACAGGACACCTCCCTGAGCGGCACTGCTG 348
QY 301 GTGTACAGGTGAAGATCTCTGGGCAACACTTCCCGCGAGCGGCCCTGATGAGAAC 360
DB 349 GTGTACAGGTGAAGATCTCTGGGCAACACTTCCCGCGAGCGGCCCTGATGAGAAC 408
QY 361 AAGGCGGCGCGCTGGGAGGCGCTCCACCGAGATGTTAGAGGTGAGACGGCGTGGCGCC 420
DB 409 AAGGCGGCGCGCTGGGAGGCGCTCCACCGAGATGTTAGAGGTGAGACGGCGTGGCGCC 468
QY 421 GGCAGATCCAGCATGAGTCCCTGAGTCCCGCGCGGTGCGCACTGACCTGCGAC 480
DB 469 GGCAGATCCCTGATGAGTCCCTGAGTCCCGCGCGGTGCGCACTGACCTGCGAC 528
QY 481 ACCACCTACCGCTCCAAAGAGCCGCTTCGCTGAGATGCGCGCTTCACTTTCGAG 540
DB 529 ACCACCTACCGCTCCAAAGAGCCGCTTCGCTGAGATGCGCGCTTCACTTTCGAG 588
QY 541 GACCAACCGGATGAGATCTCTGAGAGGAGTGGAGAAAGGCAAGTGTACAAAGATGACGAG 600
DB 589 GACCAACCGGATGAGATCTCTGAGAGGAGTGGAGAAAGGCAAGTGTACAAAGATGACGAG 648
QY 601 GCCGCGGTGGGCGGTACTGCGACGCGCGCCCTCCAAAGCTGGGCGCAACTGGA 654
DB 649 GCCGCGGTGGGCGGTACTGCGACGCGCGCCCTCCAAAGCTGGGCGCAACTGGA 702

RESULT 4
US-10-081-864-21
; Sequence 21, Application US/10081864
; Publication No. US20030022287A1
; GENERAL INFORMATION:
; APPLICANT: Lukyanov, Sergey
; APPLICANT: Lukyanov, Konstantin
; APPLICANT: Yarushevich, Yuriy
; APPLICANT: Savitsky, Alexandr
; APPLICANT: Pradkov, Arcady
; TITLE OF INVENTION: No. US20030022287A1 Aggregating Fluorescent Proteins and
; FILE REFERENCE: CLON-067
; CURRENT APPLICATION NUMBER: US/10/081,864
; CURRENT FILING DATE: 2002-06-19
```

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; PRIOR APPLICATION NUMBER: 10/006,922
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/270,983
; PRIOR FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FaSTSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 707
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: non-aggregating mutant
US-10-081-864-21

Query Match      99.3%; Score 649.2; DB 14; Length 707;
Best Local Similarity 99.5%; Pred. No. 7.3e-153;
Matches 651; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAGGGGACCGGTGAAGGCGCACTACTTCAAGTGACCGGCAAGGGCGAAGGGCAACCCCTTC 60
DB 49 GAGGGGACCGGTGAAGGCGCACTACTTCAAGTGACCGGCAAGGGCGAAGGGCAACCCCTTC 108
QY 61 GAGGGGACCGGTGAAGGCGCACTACTTCAAGTGACCGGCGGCGCCCTTCCGCTTC 120
DB 109 GAGGGGACCGGTGAAGGCGCACTACTTCAAGTGACCGGCGGCGCCCTTCCGCTTC 168
QY 121 CACATCTGTCCACTCTCTGATGATGAGGCTCCAGGCTTCATCAAGTACGTTCGGGC 180
DB 169 CACATCTGTCCACTCTCTGATGATGAGGCTCCAGGCTTCATCAAGTACGTTCGGGC 228
QY 181 ATCCCGACTACTTCAAGGAGTCCCTCCCGAGGGCTTCACTGGAGGCGCAACCAACC 240
DB 229 ATCCCGACTACTTCAAGGAGTCCCTCCCGAGGGCTTCACTGGAGGCGCAACCAACC 288
QY 241 TACGAGGACGGGCGCTTCTGACCGGCCACAGGACACCTCCCTGAGCGGCACTGCTG 300
DB 289 TACGAGGACGGGCGCTTCTGACCGGCCACAGGACACCTCCCTGAGCGGCACTGCTG 348
QY 301 GTGTACAGGTGAAGATCTCTGGGCAACACTTCCCGCGAGCGGCCCTGATGAGAAC 360
DB 349 GTGTACAGGTGAAGATCTCTGGGCAACACTTCCCGCGAGCGGCCCTGATGAGAAC 408
QY 361 AAGGCGGCGCGCTGGGAGGCGCTCCACCGAGATGTTAGAGGTGAGACGGCGTGGCGCC 420
DB 409 AAGGCGGCGCGCTGGGAGGCGCTCCACCGAGATGTTAGAGGTGAGACGGCGTGGCGCC 468
QY 421 GGCAGATCCAGCATGAGTCCCTGAGTCCCGCGCGGTGCGCACTGACCTGCGAC 480
DB 469 GGCAGATCCCTGATGAGTCCCTGAGTCCCGCGCGGTGCGCACTGACCTGCGAC 528
QY 481 ACCACCTACCGCTCCAAAGAGCCGCTTCGCTGAGATGCGCGCTTCACTTTCGAG 540
DB 529 ACCACCTACCGCTCCAAAGAGCCGCTTCGCTGAGATGCGCGCTTCACTTTCGAG 588
QY 541 GACCAACCGGATGAGATCTCTGAGAGGAGTGGAGAAAGGCAAGTGTACAAAGATGACGAG 600
DB 589 GACCAACCGGATGAGATCTCTGAGAGGAGTGGAGAAAGGCAAGTGTACAAAGATGACGAG 648
QY 601 GCCGCGGTGGGCGGTACTGCGACGCGCGCCCTCCAAAGCTGGGCGCAACTGGA 654
DB 649 GCCGCGGTGGGCGGTACTGCGACGCGCGCCCTCCAAAGCTGGGCGCAACTGGA 702

RESULT 5
US-10-806-930-9
; Sequence 9, Application US/10806930
; Publication No. US20040216180A1
; GENERAL INFORMATION:
; APPLICANT: Lukyanov, Sergey
; APPLICANT: Nucleic Acids Encoding Linked
; TITLE OF INVENTION: Chromo/Fluorescent Domains and Methods for Using the Same
; FILE REFERENCE: CLON-094
; CURRENT APPLICATION NUMBER: US/10/806,930
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; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: 09/976,673
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/356,225
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/383,336
; PRIOR FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: PCT/US02/32560
; PRIOR FILING DATE: 2002-10-10
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1398
; TYPE: DNA
; ORGANISM: Anthozoa
US-10-806-930-9

Query Match          99.0%   Score 647.6, DB 18, Length 1398,
Best Local Similarity 99.4%   Pred. No.1,8e-152,
Matches 650, Conservative 0, Mismatches 4, Indels 0, Gaps 0,

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Db	43	GAGGGCA	CCG	GTAA	CGG	CACTA	CTT	CA	GTG	CA	CGG	CA	AGG	GC	AAGG	CA	CC	CTC	102
OY	61	GAGGGCA	CC	CA	GAG	TGA	AGAT	CGA	GGT	GA	TGA	GGG	CGG	CC	CC	CTG	CC	CTT	120
Db	103	GAGGGCA	CC	CA	GAG	TGA	AGAT	CGA	GGT	GA	TGA	GGG	CGG	CC	CC	CTG	CC	CTT	162
OY	121	CACAT	CTG	TCA	CGC	CT	CG	CA	TG	AGG	CTT	CA	TCA	AGT	AC	TG	CC	GGC	180
Db	163	CACAT	CTG	TCA	CGC	CT	CG	CA	TG	AGG	CTT	CA	TCA	AGT	AC	TG	CC	GGC	222
OY	181	ATCCCGA	CTA	CTT	CA	GCA	GTCC	CT	CC	CGA	GGG	CTT	CA	CTT	GGG	AG	CA	CA	240
Db	223	ATCCCGA	CTA	CTT	CA	GCA	GTCC	CT	CC	CGA	GGG	CTT	CA	CTT	GGG	AG	CA	CA	282
OY	241	TACGAGA	CGG	CGG	CTT	CT	GA	CCG	CC	CA	CA	GGA	CAC	CT	CC	TGA	CGG	CGA	300
Db	283	TACGAGA	CGG	CGG	CTT	CT	GA	CCG	CC	CA	CA	GGA	CAC	CT	CC	TGA	CGG	CGA	342
OY	301	GTTGTA	CA	AGT	GA	AAAT	CT	CT	GGG	CA	CA	CTT	CC	CC	CGA	CGG	CC	CGT	360
Db	343	GTTGTA	CA	AGT	GA	AAAT	CT	CT	GGG	CA	CA	CTT	CC	CC	CGA	CGG	CC	CGT	402
OY	361	AAGCG	CGG	CGG	CT	TGA	AGC	CTT	CA	CGA	AT	GT	GA	CGA	GTG	AG	CGG	CT	420
Db	403	AAGCG	CGG	CGG	CT	TGA	AGC	CTT	CA	CGA	AT	GT	GA	CGA	GTG	AG	CGG	CT	462
OY	421	GGCGA	GT	CA	GAT	ATGG	CC	CT	TGA	AGT	GC	CC	CGG	CG	CGA	CTT	GA	CT	480
Db	463	GGCGA	GT	CA	GAT	ATGG	CC	CT	TGA	AGT	GC	CC	CGG	CG	CGA	CTT	GA	CT	522
OY	481	ACCA	CTT	AC	CGT	CCA	GA	AGC	CGG	CTT	CGG	CT	GA	AT	GC	CGG	CTT	CA	540
Db	523	ACCA	CTT	AC	CGT	CCA	GA	AGC	CGG	CTT	CGG	CT	GA	AT	GC	CGG	CTT	CA	582
OY	541	GACCA	CGG	CA	TG	AAT	CT	TGA	AGA	GGT	GA	AGG	GA	AGG	GA	ATG	CT	CA	600
Db	583	GACCA	CGG	CA	TG	AAT	CT	TGA	AGA	GGT	GA	AGG	GA	AGG	GA	ATG	CT	CA	642
OY	601	GCCG	CGT	GGG	CGG	TA	CTG	CGA	CGC	CGC	CT	CC	CA	AGT	GGG	CA	CA	CT	654
Db	643	GCCG	CGT	GGG	CGG	TA	CTG	CGA	CGC	CGC	CT	CC	CA	AGT	GGG	CA	CA	CT	696

RESULT 6
US-10-006-922-41
; Sequence 41, Application US/10006922
; Publication No. US20020197676a1
; GENERAL INFORMATION:
; APPLICANT: Lukyanov, Sergey A
; APPLICANT: Frakov, Arcady F.

```

/ APPLICANT: Labas, Yulii A.
/ APPLICANT: Matcz, Mikhail V.
/ APPLICANT: Terskikh, Alexey
/ TITLE OF INVENTION: No. US20020197676A1 Chromophores/Fluorophores and
/ TITLE OF INVENTION: Methode for Using the Same
/ FILE REFERENCE: CLON-035C1P
/ CURRENT APPLICATION NUMBER: US/10/006,922
/ CURRENT FILING DATE: 2001-12-04
/ PRIOR APPLICATION NUMBER: 09/150,330
/ PRIOR FILING DATE: 1998-12-11
/ PRIOR APPLICATION NUMBER: 09/457,998
/ PRIOR FILING DATE: 1999-12-09
/ PRIOR APPLICATION NUMBER: 09/458,144
/ PRIOR FILING DATE: 1999-12-09
/ PRIOR APPLICATION NUMBER: 09/458,477
/ PRIOR FILING DATE: 1999-12-09
/ PRIOR APPLICATION NUMBER: 09/457,556
/ PRIOR FILING DATE: 1999-12-09
/ PRIOR APPLICATION NUMBER: 09/444,338
/ PRIOR FILING DATE: 1999-11-19
/ NUMBER OF SEQ ID NOS: 46
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 41
/ LENGTH: 699
/ TYPE: DNA
/ ORGANISM: Anemonia sulcata
US-10-006-922-41

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[illegible]

Db 646 GCCGCGGTGGCGGCTACTGCGACGCCGCCCTCCAGCTGGGCCAACAATA 699

RESULT 7
US-10-724-178-17
; Sequence 17, Application US/10724178
; Publication No. US20040137528A1
; GENERAL INFORMATION:
; APPLICANT: Odysey Thera, Inc.
; APPLICANT: Michnick, Stephen
; APPLICANT: Macdonald, Marlie
; APPLICANT: Lamerdin, Jane
; TITLE OF INVENTION: FRAGMENTS OF FLUORESCENT PROTEINS FOR PROTEIN-FRAGMENT
; FILE REFERENCE: ODDY007
; CURRENT APPLICATION NUMBER: US/10/724,178
; CURRENT FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: US 60/461,133
; PRIOR FILING DATE: 2003-04-09
; NUMBER OF SEQ ID NOS: 1067
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 696
; TYPE: DNA
; ORGANISM: Artificial
; OTHER INFORMATION: "KPPI" a mutated variant of kindling fluorescent protein ascp frc
; FEATURE:
; OTHER INFORMATION: m. A. sulcata
; NAME/KEY: CDS
; LOCATION: (1)..(696)
US-10-724-178-17

Query Match 95.4%; Score 623.8; DB 18; Length 696;
Best Local Similarity 97.4%; Pred. No. 1.6e-146;
Matches 634; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 1 GAGGGGACCGGTGAACGGCCCACTTCAAGTGCACGGGCAAGGGGCAACCCCTTC 60
DB 46 GAGGGGACCGGTGAACGGCCCACTGCTCAAGTGCATGGGCAAGGGGCAACCCCTTC 105
QY 61 GAGGGGACCGGAGATGAAGATCGAGTGAAGGGGGGGGGGGGGGGGGGGGGGGGG 120
DB 106 GAGGGGACCGGAGATGAAGATCGAGTGAAGGGGGGGGGGGGGGGGGGGGGGGGG 165
QY 121 CACATCTGTCACTCTCGATGATCGAGTCCCAAGGCTTCACTCAAGTACGTGCGGG 180
DB 166 CACATCTGTCACTCTCGATGATCGAGTCCCAAGGCTTCACTCAAGTACGTGCGGG 225
QY 181 ATCCCGGACTTCACTTCAAGAGTCTCTCCCGAGGGCTTCACTGGAGGGGCAACACC 240
DB 226 ATCCCGGACTTCACTTCAAGAGTCTCTCCCGAGGGCTTCACTGGAGGGGCAACACC 285
QY 241 TACGAGAGCGGGGGCTTCTCGACCGGCAACAGACACCTCCCTGGACGGGCACTGG 300
DB 286 TACGAGAGCGGGGGCTTCTCGACCGGCAACAGACACCTCCCTGGACGGGCACTGG 345
QY 301 GTGTACAGAGTGAAGATCTCTGGGCAAACTTCCCGCGGACGGCCCGGTGATGCAAG 360
DB 346 GTGTACAGAGTGAAGATCTCTGGGTAACAATTCCCGCGGACGGCCCGGTGATGCAAG 405
QY 361 AAGGGCGGGGGCTTCTCGACCGGCAACAGATGTGTAGAGGTGACGGCGTGTGCGG 420
DB 406 AAGGTGCGGGGGCTTCTCGACCGGCAACAGATGTGTAGAGGTGACGGCGTGTGCGG 465
QY 421 GGGCACTCCAGATGAGCGCTTCAAGAGTCCCGGGGCTGCGCACTGACCTGGCACTG 480
DB 466 GGGCACTCCAGATGAGCGCTTCAAGAGTCCCGGGGCTGCGCACTGACCTGGCACTG 525
QY 481 ACCACCTACCGCTCAAGAAAGCCGGCTTCGCTGTAAGATGCGGGCTTTCATTGAG 540
DB 526 ACCACCTACCGCTCAAGAAAGCCGGCTTCGCTGTAAGATGCGGGCTTTCATTGAG 585

QY 541 GACCAACCGGATGAGATCTCTGAGAGGTGAGAAAGGGCAAGTCTCAACAGATACGAG 600
DB 586 GACCAACCGGATGAGATCTCTGAGAGGTGAGAAAGGGCAAGTCTCAACAGATACGAG 645

QY 601 GCCGCGGTGGCGGCTACTGCGACGCCGCCCTCCAGCTGGGGCAACAAC 651
DB 646 GCCGCGGTGGCGGCTACTGCGACGCCGCCCTCCAGCTGGGGCAACAAC 696

RESULT 8
US-10-724-178-1046
; Sequence 1046, Application US/10724178
; Publication No. US20040137528A1
; GENERAL INFORMATION:
; APPLICANT: Odysey Thera, Inc.
; APPLICANT: Michnick, Stephen
; APPLICANT: Macdonald, Marlie
; APPLICANT: Lamerdin, Jane
; TITLE OF INVENTION: FRAGMENTS OF FLUORESCENT PROTEINS FOR PROTEIN-FRAGMENT
; FILE REFERENCE: ODDY007
; CURRENT APPLICATION NUMBER: US/10/724,178
; CURRENT FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: US 60/461,133
; PRIOR FILING DATE: 2003-04-09
; NUMBER OF SEQ ID NOS: 1067
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1046
; LENGTH: 591
; TYPE: DNA
; ORGANISM: Artificial
; OTHER INFORMATION: modif. frag.; KFP F2A, with Met added @ position 1
; FEATURE:
; OTHER INFORMATION: m. A. sulcata
; NAME/KEY: CDS
; LOCATION: (1)..(591)
; OTHER INFORMATION: KFP F2A corresponds to aa residues 37-end of KPPI
US-10-724-178-1046

Query Match 86.6%; Score 566.6; DB 18; Length 591;
Best Local Similarity 97.6%; Pred. No. 3.3e-132;
Matches 575; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 63 GGGGACCGGAGATGAAGATGAGGTGATGAGGGGGGGGGGGGGGGGGGGGGGGGG 122
DB 3 GGGGACCGGAGATGAAGATGAGGTGATGAGGGGGGGGGGGGGGGGGGGGGGGGG 62
QY 123 CATCTGTCACTCTCTGATGATGAGGTCCCAAGGCTTCACTCAAGTACGTGCGGGCAT 182
DB 63 CATCTGTCACTCTCTGATGATGAGGTCCCAAGGCTTCACTCAAGTACGTGCGGGCAT 122
QY 183 CCCGCACTACTTCAAGAGTCTCTCCCGAGGGCTTCACTGGAGGGGCAACCACTTA 242
DB 123 CCCGCACTACTTCAAGAGTCTCTCCCGAGGGCTTCACTGGAGGGGCAACCACTTA 182
QY 243 CGAGAGCGGGGGCTTCTCGACCGGCAACAGACACCTCCCTGGAGGGGCACTGG 302
DB 183 CGAGAGCGGGGGCTTCTCGACCGGCAACAGACACCTCCCTGGAGGGGCACTGG 242
QY 303 GTACAGAGTGAAGATCTCTGGGCAAACTTCCCGCGGACGGCCCGGTGATGCAAG 362
DB 243 GTACAGAGTGAAGATCTCTGGGTAACAATTCCCGCGGACGGCCCGGTGATGCAAG 302
QY 363 GGGCGGGGGCTTCTCGACCGGCAACAGATGTGTAGAGGTGACGGCGTGTGCGG 422
DB 303 GGTGCGGGGGCTTCTCGACCGGCAACAGATGTGTAGAGGTGACGGCGTGTGCGG 362
QY 423 CGAGTTCAGAGTGGCGCTTCAAGAGTCCCGGGGCTGCGCACTGACCTGGCACTG 482
DB 363 CGAGTTCAGAGTGGCGCTTCAAGAGTCCCGGGGCTGCGCACTGACCTGGCACTG 422
QY 483 CACTTACCGCTCAAGAAAGCCGGCTTCGCTGTAAGATGCGGGCTTTCATTGAGAG 542

Db 423 CACCTACCGCTCAAGAGCCGCTCCGCTTGAAGTCCGCTTCACTTGAAGA 482
Qy 543 CCACCGCATCGAGATCTCGAGAGAGTGAGAGAGGCAAGTCTCAAGCACTAGAGGC 602
Db 483 CCACCGCATCGAGATCTCGAGAGAGTGAGAGAGGCAAGTCTCAAGCACTAGAGGC 542
Qy 603 CGCGGTGGGCGCTACTGCGAGCGCGCCCTTCAAGCTGGGCGCAAC 651
Db 543 CGCGGTGGGCGCTACTGCGAGCGCGCCCTTCAAGCTGGGCGCAAC 591

RESULT 9

US-10-724-178-1064
; Sequence 1064, Application US/10724178
; Publication No. US20040137528A1
; GENERAL INFORMATION:
; APPLICANT: Odyssey Thera, Inc.
; APPLICANT: Michael, Stephen
; APPLICANT: Macdonald, Marnie
; APPLICANT: Lamerdin, Jane
; TITLE OF INVENTION: FRAGMENTS OF FLUORESCENT PROTEINS FOR PROTEIN-FRAGMENT
; FILE REFERENCE: ODDY007
; CURRENT APPLICATION NUMBER: US/10/724,178
; CURRENT FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: US 60/461,133
; PRIOR FILING DATE: 2003-04-09
; NUMBER OF SEQ ID NOS: 1067
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1064
; LENGTH: 555
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: modif. frag.; KFP F1F, with position 1 Met removed
; NAME/KEY: CDS
; LOCATION: (1)..(555)
; OTHER INFORMATION: KFP F1F corresponds to aa residues 1-186 of KFP1
US-10-724-178-1064

Query Match 74.5%; Score 487.4; DB 18; Length 555;
Best Local Similarity 96.9%; Pred. No. 2.2e-112;
Matches 497; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
Qy 1 GAGGGCAACCGTGAACGGCACTACTCAAGTCAACCGGCAAGGAGAGGCAACCCCTC 60
Db 43 GAGGGCAACCGTGAACGGCACTACTCAAGTCAACCGGCAAGGAGAGGCAACCCCTC 102
Qy 61 GAGGGCAACCGTGAACGGCACTACTCAAGTCAACCGGCAAGGAGAGGCAACCCCTC 120
Db 103 GAGGGCAACCGTGAACGGCACTACTCAAGTCAACCGGCAAGGAGAGGCAACCCCTC 162
Qy 121 CACATCTGTCACTCTCTGATGATGAGGCTTCAAGGCTTCAATCAAGTACGTGCGGC 180
Db 163 CACATCTGTCACTCTCTGATGATGAGGCTTCAAGGCTTCAATCAAGTACGTGCGGC 222
Qy 181 ATCCCGACTACTTCAAGCAAGTCCCTCCGAGGGCTTCACTGGAGCGGACCAACACC 240
Db 223 ATCCCGACTACTTCAAGCAAGTCCCTCCGAGGGCTTCACTGGAGCGGACCAACACC 282
Qy 241 TACGAGACGGCGGCTTCTGACCGCCCAACGAGCACTCTCCGTGAGCGGAGCTGCTG 300
Db 283 TACGAGACGGCGGCTTCTGACCGCCCAACGAGCACTCTCCGTGAGCGGAGCTGCTG 342
Qy 301 GTGTACAAGGTGAAGATCTGGGCAACAATTCCCGCGAGCGGCCGTGATGAGAAC 360
Db 343 GTGTACAAGGTGAAGATCTGGGCAACAATTCCCGCGAGCGGCCGTGATGAGAAC 402
Qy 361 AAGGCGGCGCTGGAGCGCTTCAACCGAGTCTGTACAGAGTGAAGCGGCTGCTGCGC 420
Db 403 AAGGCGGCGCTGGAGCGCTTCAACCGAGTCTGTACAGAGTGAAGCGGCTGCTGCGC 462

Qy 421 GAGGAGTCCAGATGCGCTTGAAGTCCCGGCGGTGCGACACTGACTGCACTGAC 480
Db 463 GAGGAGTCCAGATGCGCTTGAAGTCCCGGCGGTGCGACACTGACTGCACTGAC 522
Qy 481 ACACCTACCGCTTCAAGAGCCGCTTCCGCGC 513
Db 523 ACACCTACCGCTTCAAGAGCCGCTTCCGCGC 555

RESULT 10

US-10-724-178-1060
; Sequence 1060, Application US/10724178
; Publication No. US20040137528A1
; GENERAL INFORMATION:
; APPLICANT: Odyssey Thera, Inc.
; APPLICANT: Michael, Stephen
; APPLICANT: Macdonald, Marnie
; APPLICANT: Lamerdin, Jane
; TITLE OF INVENTION: FRAGMENTS OF FLUORESCENT PROTEINS FOR PROTEIN-FRAGMENT
; FILE REFERENCE: ODDY007
; CURRENT APPLICATION NUMBER: US/10/724,178
; CURRENT FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: US 60/461,133
; PRIOR FILING DATE: 2003-04-09
; NUMBER OF SEQ ID NOS: 1067
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1060
; LENGTH: 504
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: modif. frag.; KFP F1B, with position 1 Met removed
; NAME/KEY: CDS
; LOCATION: (1)..(504)
; OTHER INFORMATION: KFP F1E corresponds to aa residues 1-169 of KFP1
US-10-724-178-1060

Query Match 66.7%; Score 436.4; DB 18; Length 504;
Best Local Similarity 96.5%; Pred. No. 1.2e-99;
Matches 446; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
Qy 1 GAGGGCAACCGTGAACGGCACTACTCAAGTCAACCGGCAAGGAGAGGCAACCCCTC 60
Db 43 GAGGGCAACCGTGAACGGCACTACTCAAGTCAACCGGCAAGGAGAGGCAACCCCTC 102
Qy 61 GAGGGCAACCGTGAACGGCACTACTCAAGTCAACCGGCAAGGAGAGGCAACCCCTC 120
Db 103 GAGGGCAACCGTGAACGGCACTACTCAAGTCAACCGGCAAGGAGAGGCAACCCCTC 162
Qy 121 CACATCTGTCACTCTCTGATGATGAGGCTTCAAGGCTTCAATCAAGTACGTGCGGC 180
Db 163 CACATCTGTCACTCTCTGATGATGAGGCTTCAAGGCTTCAATCAAGTACGTGCGGC 222
Qy 181 ATCCCGACTACTTCAAGCAAGTCCCTCCGAGGGCTTCACTGGAGCGGACCAACACC 240
Db 223 ATCCCGACTACTTCAAGCAAGTCCCTCCGAGGGCTTCACTGGAGCGGACCAACACC 282
Qy 241 TACGAGACGGCGGCTTCTGACCGCCCAACGAGCACTCTCCGTGAGCGGAGCTGCTG 300
Db 283 TACGAGACGGCGGCTTCTGACCGCCCAACGAGCACTCTCCGTGAGCGGAGCTGCTG 342
Qy 301 GTGTACAAGGTGAAGATCTGGGCAACAATTCCCGCGAGCGGCCGTGATGAGAAC 360
Db 343 GTGTACAAGGTGAAGATCTGGGCAACAATTCCCGCGAGCGGCCGTGATGAGAAC 402
Qy 361 AAGGCGGCGCTGGAGCGCTTCAACCGAGTCTGTACAGAGTGAAGCGGCTGCTGCGC 420
Db 403 AAGGCGGCGCTGGAGCGCTTCAACCGAGTCTGTACAGAGTGAAGCGGCTGCTGCGC 462
Qy 421 GAGGAGTCCAGATGCGCTTGAAGTCCCGGCGGTGCGACACTGACTGCACTGAC 480


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Db      294 ATTCCTGACTTACTTCAAGCAGTCTTTCCCTGAGAGTTTACTTGAGAAAGAACACACACC 353
Qy      241 TACGAGAGCGGCGCTTCTCTGAACCGCCACCAAGACACCTCCCTGAGCGGCGACTGCG 300
Db      354 TACGAGGATGAGGCTTTCTTACAGCTCATCAGAGACAAAGCTTAGATGAGATTGCTTC 413
Qy      301 GTGTACAGAGTGAAGATCTGTGGCAACAATTCCCGCCGACGAGCCCTGTATGCGAAGC 360
Db      414 GTTTACAAAGTCAAGATTTCTTGATATATATTTTCTGCTGATGAGCCCTGTAGACAGAAC 473
Qy      361 AAGGCGGCGCGCTGGAGAGCCCTCCACCGAGATGATGATGAGAGGTGAGACGGCGTGCAGC 420
Db      474 AAGCAGGAGATGAGAGGACCAAGCAGCAGATGATTTAGAGATTGACGGTGTCTGCGT 533
Qy      421 GGCAGTCCAGCATGAGCCCTGAGAGTCCCGCGGCGTGCACCTGACCTGCACCTGCAC 480
Db      534 GGAACAGTCTTTGATGAGCCCTTAAGTGCCTGAGTGTGATCATCTGACTTGCCATCTCCAT 593
Qy      481 ACCACTTACCGCTCCAGAAAGCCCGCTCGCTGAAATGCGCGGCTTCCACTTCGAG 540
Db      594 ACTACTTACAGGTCCAAAAAACAGAGTATGCTTGAAGATGCGCAGATTTTCAATTTGAA 653
Qy      541 GACCAACCGATGAGATCCGTGAGAGAGTGGAGAGGCGCAAGTGTACAAGCAGTACGAG 600
Db      654 GATCATCGCATCGAGATTAATGAGAGAGTTTGAGAAAGGCAAGTGTCTATTAACGATACGA 713
Qy      601 GCCGCGTGGCGCGCTACTGCGAGCGCGCCCTCCAACTGAGGCCAACCTGA 654
Db      714 GCAGCAGTGGGAGGTAAGTGTGATGTGCTGCTCCATCCAACTTGAATTAATCTAA 767

RESULT 15
; Sequence 5, Application US/10155809
; Publication No. US20030092884A1
; GENERAL INFORMATION:
; APPLICANT: Lukyanov, Sergey
; APPLICANT: Chudakov, Dmitry
; TITLE OF INVENTION: Kindling Fluorescent Proteins and
; FILE REFERENCE: CION-073
; CURRENT APPLICATION NUMBER: US/10/155,809
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 60/293,752
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/329,176
; PRIOR FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: 10/006,922
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 09/210,330
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: 09/976,673
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PaSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 767
; TYPE: DNA
; ORGANISM: anthozoa
US-10-155-809-5

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Query Match 62.6%; Score 409.2; DB 14; Length 767;
 Best Local Similarity 76.6%; Pired. No. 7.8e-93;
 Matches 501; Conservative 0; Mismatches 153; Indels 0; Gaps 0;

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Qy      1 GAGGGACCGTGAACGGCCACTTCAAGTSCACCGGAGGCGAGGGCAACCCCTTC 60
Db      114 GAAAGGACGGTATATGCGCACTACTTCAAGTACAGAAAGAGGGCAACCAATTT 173
Qy      61 GAGGGACCGCAGAGATGAAGATCGAGGTATGAGGGCGGCCCTTGCCCTTGCCCTTC 120

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Db      174 GAGGGTACGAGAAATGATAGAGTATGAGTATGAGAGAGTCCATTTGCTTC 233
Qy      121 CACATCTCTCTCACTCTCTGCAATGACGCTTCAAGGCTTCAATCAAGTATGCTTCGGC 180
Db      234 CACATTTGTCTCAACGAGTGTATGACGATAGATAGACCTTCAATCAAGTATGCTCAGGA 293
Qy      181 ATCCCGACTTACTTCAAGAGTCCCTCCCGAGGAGGCTTCACTGAGGAGGCGACACACC 240
Db      294 ATTCCTGACTTACTTCAAGCAGTCTTTCCCTGAGAGTCTTACTTGAGAAAGAACACACACC 353
Qy      241 TACGAGAGCGGCGCTTCTCTGAACCGCCACCAAGACACCTCCCTGAGCGGCGACTGCG 300
Db      354 TACGAGGATGAGGCTTTCTTACAGCTCATCAGAGACAAAGCTTAGATGAGATTGCTTC 413
Qy      301 GTGTACAGAGTGAAGATCTGTGGCAACAATTCCCGCCGACGAGCCCTGTATGCGAAGC 360
Db      414 GTTTACAAAGTCAAGATTTCTTGATATATATTTTCTGCTGATGAGCCCTGTATGCGAAGC 473
Qy      361 AAGGCGGCGCGCTGGAGAGCCCTCCACCGAGATGATGATGAGAGGTGAGACGGCGTGCAGC 420
Db      474 AAGCAGGAGATGAGAGGACCAAGCAGCAGATGATTTAGAGATTGACGGTGTCTGCGT 533
Qy      421 GGCAGTCCAGCATGAGCCCTGAGAGTCCCGCGGCGTGCACCTGACCTGCACCTGCAC 480
Db      534 GGAACAGTCTTTGATGAGCCCTTAAGTGCCTGAGTGTGATCATCTGACTTGCCATCTCCAT 593
Qy      481 ACCACTTACCGCTCCAGAAAGCCCGCTCGCTGAAATGCGCGGCTTCCACTTCGAG 540
Db      594 ACTACTTACAGGTCCAAAAAACAGAGTATGCTTGAAGATGCGCAGATTTTCAATTTGAA 653
Qy      541 GACCAACCGATGAGATCCGTGAGAGAGTGGAGAGGCGCAAGTGTACAAGCAGTACGAG 600
Db      654 GATTAACCGCATCGAGATTAATGAGAGAGTTTGAGAAAGGCAAGTGTCTATTAACGATACGA 713
Qy      601 GCCGCGTGGCGCGCTACTGCGAGCGCGCCCTCCAACTGAGGCCAACCTGA 654
Db      714 GCAGCAGTGGGAGGTAAGTGTGATGTGCTGCTCCATCCAACTTGAATTAATCTAA 767

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Search completed: May 29, 2005, 23:53:10
 Job time : 529.342 secs

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